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(54) Title: G PROTEIN-COUPLED RECEPTORS EXPRESSED IN BRAIN

(57) Abstract: The present invention provides genes encoding heretofore unknown G protein-coupled receptors, constructs and recombinant host cells incorporating the genes; the GPCR polypeptides encoded by the genes; antibodies to the polypeptides; and methods of making and using all of the foregoing.

WO 01/31014 A2

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- 1 -

G PROTEIN-COUPLED RECEPTORS EXPRESSED IN BRAIN

RELATED APPLICATIONS

This patent application is a continuation-in-part of the following U.S. patent applications: Serial No. 09/481,794 filed January 12, 2000; Serial No. 09/454,399 filed December 3, 1999; Serial Nos. 09/429,517, 09/429,555, 09/429,676, 09/429,695 filed October 28, 1999; and Serial Nos. 09/428,114, 09/428,020, 09/427,859 and 09/427,653 filed October 27, 1999. All these application are incorporated herein by reference.

FIELD OF THE INVENTION

The present invention relates generally to the fields of genetics and cellular and molecular biology. More particularly, the invention relates to a novel G protein-coupled seven transmembrane receptor polynucleotide and polypeptide sequences that are expressed in the brain.

DESCRIPTION OF RELATED ART

Humans and other life forms are comprised of living cells. Among the mechanisms through which the cells of an organism communicate with each other and obtain information and stimuli from their environment is through cell membrane receptor molecules expressed on the cell surface. Many such receptors have been identified, characterized, and sometimes classified into major receptor superfamilies based on structural motifs and signal transduction features. Such families include (but are not limited to) ligand-gated ion channel receptors, voltage-dependent ion channel receptors, receptor tyrosine kinases, receptor protein tyrosine phosphatases, and G protein-coupled receptors. The receptors are a first essential link for translating an extracellular signal into a cellular physiological response.

The G protein-coupled receptors (GPCR) form a vast superfamily of cell surface receptors which are characterized by an amino-terminal extracellular domain, a carboxyl-terminal intracellular domain, and a serpentine structure that passes through the cell membrane seven times. Hence, such receptors are sometimes also referred to as seven transmembrane (7TM) receptors. These seven

- 2 -

transmembrane domains define three extracellular loops and three intracellular loops, in addition to the amino- and carboxyl-terminal domains. The extracellular portions of the receptor have a role in recognizing and binding one or more extracellular binding partners (ligands), whereas the intracellular portions have a role in recognizing and communicating with downstream effector molecules.

The G protein-coupled receptors bind a variety of ligands including calcium ions, hormones, chemokines, neuropeptides, neurotransmitters, nucleotides, lipids, odorants, and even photons, and are important in the normal (and sometimes the aberrant) function of many cell types. [See generally A.D. Strosberg, *Eur. J. Biochem.*, 196: 1-10 (1991) and S. K. Bohm *et al.*, *Biochem J.*, 322: 1-18 (1997).] When a specific ligand binds to its corresponding receptor, the ligand stimulates the receptor to activate a specific heterotrimeric guanine-nucleotide-binding regulatory protein (G-protein) that is coupled to the intracellular portion of the receptor. The G protein in turn transmits a signal to an effector molecule within the cell, by either stimulating or inhibiting the activity of that effector molecule. These effector molecules include adenylate cyclase, phospholipases, and ion channels. Adenylate cyclase and phospholipases are enzymes that are involved in the production of the second messenger molecules cAMP, inositol triphosphate and diacylglycerol. It is through this sequence of events that an extracellular ligand stimuli exerts intracellular changes through a G protein-coupled receptor. Each such receptor has its own characteristic primary structure, expression pattern, ligand-binding profile, and intracellular effector system.

Because of the vital role of G protein-coupled receptors in the communication between cells and their environment, such receptors are attractive targets for therapeutic intervention, and many drugs have been registered which are directed towards activating or antagonizing such receptors. For receptors having a known ligand, the identification of agonists or antagonists may be sought specifically for enhancing or inhibiting the action of the ligand. Some G protein-coupled receptors have roles in disease pathogenesis (e.g., certain chemokine receptors that act as HIV co-receptors and may have a role in AIDS pathogenesis), and are attractive targets for therapeutic intervention even in the absence of knowledge of the natural

- 3 -

ligand of the receptor. Other receptors are attractive targets for therapeutic intervention by virtue of their expression pattern in tissues or cell types that are attractive targets for therapeutic intervention. Examples of this latter category of receptors include receptors expressed in immune cells, for targeting to enhance
5 immune responses to fight pathogens or cancer or inhibit autoimmune responses; and receptors expressed in the brain or other neurons, for targeting to treat schizophrenia, depression, bipolar disease, or other neurological disorders. This latter category of receptor is also useful as a marker for identifying and/or purifying (*e.g.*, via fluorescence activated cell sorting) cellular subtypes that express the receptor.
10 Unfortunately, only a limited number of G protein receptors from the central nervous system (CNS) are known. A need exists for identifying the existence and structure of such G protein-coupled receptors.

SUMMARY OF THE INVENTION

15 The present invention addresses one or more of the needs identified above in that it provides purified polynucleotides encoding heretofore unknown G protein-coupled receptors (GPCR); constructs and recombinant host cells incorporating the polynucleotides; GPCR polypeptides encoded by the polynucleotides; antibodies to the polypeptides; and methods of making and using all
20 of the foregoing. As set forth in detail herein, the GPCR polypeptides described herein are expressed in the brain, providing a therapeutic indication for GPCR polypeptides and binding partners to treat diseases associated with this tissue.

The invention provides purified and isolated GPCR seven transmembrane receptor polypeptides comprising any one of the amino acid
25 sequences set forth in SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18 or 20, or a fragment thereof comprising an epitope specific to the seven transmembrane receptor. By "epitope specific to" is meant a portion of the receptor that is recognizable by an antibody that is specific for that seven transmembrane receptor, as defined in detail below.

30 One preferred embodiment comprises a purified and isolated polypeptide designated CON193, comprising the complete amino acid sequence set

- 4 -

forth in SEQ ID NO: 2. This amino acid sequence was deduced from a polynucleotide sequence encoding CON193 (SEQ ID NO:1), as set forth below:

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ntggttggtg gaccattaaa atgcattatg gaatttttaa aagttggggg agagggagac 60
agtaaaaata acctatatatt tctcttggtt tttttttttt aactctagga aagcccagac 120
5 aaattttgag ctatttcata acctaccaga cttatc atg cta aca ctg aat aaa 174
                                     Met Leu Thr Leu Asn Lys
                                     1         5

aca gac cta ata cca gct tca ttt att ctg aat gga gtc cca gga ctg 222
Thr Asp Leu Ile Pro Ala Ser Phe Ile Leu Asn Gly Val Pro Gly Leu
10      10      15      20
gaa gac aca caa ctc tgg att tcc ttc cca ttc tgc tct atg tat gtt 270
Glu Asp Thr Gln Leu Trp Ile Ser Phe Pro Phe Cys Ser Met Tyr Val
      25      30      35
gtg gct atg gta ggg aat tgt gga ctc ctc tac ctc att cac tat gag 318
15 Val Ala Met Val Gly Asn Cys Gly Leu Leu Tyr Leu Ile His Tyr Glu
      40      45      50
gat gcc ctg cac aaa ccc atg tac tac ttc ttg gcc atg ctt tcc ttt 366
Asp Ala Leu His Lys Pro Met Tyr Tyr Phe Leu Ala Met Leu Ser Phe
      55      60      65      70
20 act gac ctt gtt atg tgc tct agt aca atc cct aaa gcc ctc tgc atc 414
Thr Asp Leu Val Met Cys Ser Ser Thr Ile Pro Lys Ala Leu Cys Ile
      75      80      85
ttc tgg ttt cat ctc aag gac att gga ttt gat gaa tgc ctt gtc cag 462
Phe Trp Phe His Leu Lys Asp Ile Gly Phe Asp Glu Cys Leu Val Gln
25      90      95      100
atg ttc ttc atc cac acc ttc aca ggg atg gag tct ggg gtg ctt atg 510
Met Phe Phe Ile His Thr Phe Thr Gly Met Glu Ser Gly Val Leu Met
      105      110      115
30 ctt atg gcc ctg gat cgc tat gtg gcc atc tgc tac ccc tta cgc tat 558
Leu Met Ala Leu Asp Arg Tyr Val Ala Ile Cys Tyr Pro Leu Arg Tyr
      120      125      130
tca act atc ctc acc aat cct gta att gca aag gtt ggg act gcc acc 606
Ser Thr Ile Leu Thr Asn Pro Val Ile Ala Lys Val Gly Thr Ala Thr
      135      140      145      150
35 ttc ctg aga ggg gta tta ctc att att ccc ttt act ttc ctc acc aag 654
Phe Leu Arg Gly Val Leu Leu Ile Ile Pro Phe Thr Phe Leu Thr Lys
      155      160      165
40 cgc ctg ccc tcc tgc aga ggc aat ata ctt ccc cat acc tac tgt gac 702
Arg Leu Pro Ser Cys Arg Gly Asn Ile Leu Pro His Thr Tyr Cys Asp
      170      175      180

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- 5 -

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cac atg tct gta gcc aaa ttg tcc tgt ggt aat gtc aag gtc aat gcc 750
His Met Ser Val Ala Lys Leu Ser Cys Gly Asn Val Lys Val Asn Ala
      185                      190                      195
atc tat ggt ctg atg gtt gcc ctc ctg att ggg ggc ttt gac ata ctg 798
Ile Tyr Gly Leu Met Val Ala Leu Leu Ile Gly Gly Phe Asp Ile Leu
      200                      205                      210
tgt atc acc atc tcc tat acc atg att ctc cgg gca gtg gtc agc ctc 846
Cys Ile Thr Ile Ser Tyr Thr Met Ile Leu Arg Ala Val Val Ser Leu
      215                      220                      225                      230
tcc tca gca gat gct cgg cag aag gcc ttt aat acc tgc act gcc cac 894
Ser Ser Ala Asp Ala Arg Gln Lys Ala Phe Asn Thr Cys Thr Ala His
      235                      240                      245
att tgt gcc att gtt ttc tcc tat act cca gct ttc ttc tcc ttc ttt 942
Ile Cys Ala Ile Val Phe Ser Tyr Thr Pro Ala Phe Phe Ser Phe Phe
      250                      255                      260
tcc cac cgc ttt ggg gaa cac ata atc ccc cct tct tgc cac atc att 990
Ser His Arg Phe Gly Glu His Ile Ile Pro Pro Ser Cys His Ile Ile
      265                      270                      275
gta gcc aat att tat ctg ctc cta cca ccc act atg aac cct att gtc 1038
Val Ala Asn Ile Tyr Leu Leu Leu Pro Pro Thr Met Asn Pro Ile Val
      280                      285                      290
tat ggg gtg aaa acc aaa cag ata cga gac tgt gtc ata agg atc ctt 1086
Tyr Gly Val Lys Thr Lys Gln Ile Arg Asp Cys Val Ile Arg Ile Leu
      295                      300                      305                      310
tca ggt tct aag gat acc aaa tcc tac agc atg tga atgaacactt 1132
Ser Gly Ser Lys Asp Thr Lys Ser Tyr Ser Met
      315                      320
gccaggagtg agaagagaag gaaagaatta cttctatttg cctcttatgc aggagttcat1192
aaaatctttc tggaagtact gtattgatca caaaatggag ttgntgact ggtgcattc 1252
caataagtac cttgggaatc tnacatcact ggaaggccca ccacatttct ataaat 1308

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Another preferred embodiment comprises a purified and isolated polypeptide designated CON166, comprising the complete amino acid sequence set forth in SEQ ID NO: 4. This amino acid sequence was deduced from a polynucleotide sequence encoding CON166 (SEQ ID NO: 3), as set forth below:

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35 atg gat gaa aca gga aat ctg aca gta tct tct gcc aca tgc cat gac 48
Met Asp Glu Thr Gly Asn Leu Thr Val Ser Ser Ala Thr Cys His Asp
      1           5           10           15
act att gat gac ttc cgc aat caa gtg tat tcc acc ttg tac tct atg 96
Thr Ile Asp Asp Phe Arg Asn Gln Val Tyr Ser Thr Leu Tyr Ser Met
40           20           25           30

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- 6 -

	atc tct gtt gta ggc ttc ttt ggc aat ggc ttt gtg ctc tat gtc ctc	144
	Ile Ser Val Val Gly Phe Phe Gly Asn Gly Phe Val Leu Tyr Val Leu	
	35 40 45	
5	ata aaa acc tat cac aag aag tca gcc ttc caa gta tac atg att aat	192
	Ile Lys Thr Tyr His Lys Lys Ser Ala Phe Gln Val Tyr Met Ile Asn	
	50 55 60	
	tta gca gta gca gat cta ctt tgt gtg tgc aca ctg cct ctc cgt gtg	240
	Leu Ala Val Ala Asp Leu Leu Cys Val Cys Thr Leu Pro Leu Arg Val	
	65 70 75 80	
10	gtc tat tat gtt cac aaa ggc att tgg ctc ttt ggt gac ttc ttg tgc	288
	Val Tyr Tyr Val His Lys Gly Ile Trp Leu Phe Gly Asp Phe Leu Cys	
	85 90 95	
	cgc ctc agc acc tat gct ttg tat gtc aac ctc tat tgt agc atc ttc	336
	Arg Leu Ser Thr Tyr Ala Leu Tyr Val Asn Leu Tyr Cys Ser Ile Phe	
15	100 105 110	
	ttt atg aca gcc atg agc ttt ttc cgg tgc att gca att gtt ttt cca	384
	Phe Met Thr Ala Met Ser Phe Phe Arg Cys Ile Ala Ile Val Phe Pro	
	115 120 125	
20	gtc cag aac att aat ttg gtt aca cag aaa aaa gcc agg ttt gtg tgt	432
	Val Gln Asn Ile Asn Leu Val Thr Gln Lys Lys Ala Arg Phe Val Cys	
	130 135 140	
	gta ggt att tgg att ttt gtg att ttg acc agt tct cca ttt cta atg	480
	Val Gly Ile Trp Ile Phe Val Ile Leu Thr Ser Ser Pro Phe Leu Met	
	145 150 155 160	
25	gcc aaa cca caa aaa gat gag aaa aat aat acc aag tgc ttt gag ccc	528
	Ala Lys Pro Gln Lys Asp Glu Lys Asn Asn Thr Lys Cys Phe Glu Pro	
	165 170 175	
	cca caa gac aat caa act aaa aat cat gtt ttg gtc ttg cat tat gtg	576
	Pro Gln Asp Asn Gln Thr Lys Asn His Val Leu Val Leu His Tyr Val	
30	180 185 190	
	tca ttg ttt gtt ggc ttt atc atc cct ttt gtt att ata att gtc tgt	624
	Ser Leu Phe Val Gly Phe Ile Ile Pro Phe Val Ile Ile Ile Val Cys	
	195 200 205	
35	tac aca atg atc att ttg acc tta cta aaa aaa tca atg aaa aaa aat	672
	Tyr Thr Met Ile Ile Leu Thr Leu Leu Lys Lys Ser Met Lys Lys Asn	
	210 215 220	
	ctg tca agt cat aaa aag gct ata gga atg atc atg gtc gtg acc gct	720
	Leu Ser Ser His Lys Lys Ala Ile Gly Met Ile Met Val Val Thr Ala	
	225 230 235 240	
40	gcc ttt tta gtc agt ttc atg cca tat cat att caa cgt acc att cac	768
	Ala Phe Leu Val Ser Phe Met Pro Tyr His Ile Gln Arg Thr Ile His	
	245 250 255	

- 7 -

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      ctt cat ttt tta cac aat gaa act aaa ccc tgt gat tct gtc ctt aga 816
      Leu His Phe Leu His Asn Glu Thr Lys Pro Cys Asp Ser Val Leu Arg
                260                265                270
      atg cag aag tcc gtg gtc ata acc ttg tct ctg gct gca tcc aat tgt 864
5      Met Gln Lys Ser Val Val Ile Thr Leu Ser Leu Ala Ala Ser Asn Cys
                275                280                285
      tgc ttt gac cct ctc cta tat ttc ttt tct ggg ggt aac ttt agg aaa 912
      Cys Phe Asp Pro Leu Leu Tyr Phe Phe Ser Gly Gly Asn Phe Arg Lys
                290                295                300
10     agg ctg tct aca ttt aga aag cat tct ttg tcc agc gtg act tat gta 960
      Arg Leu Ser Thr Phe Arg Lys His Ser Leu Ser Ser Val Thr Tyr Val
      305                310                315                320
      ccc aga aag aag gcc tct ttg cca gaa aaa gga gaa gaa ata tgt aaa 1008
      Pro Arg Lys Lys Ala Ser Leu Pro Glu Lys Gly Glu Glu Ile Cys Lys
15     gta tag                325                330                335
      Val
      1014

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Still another preferred embodiment comprises a purified and isolated polypeptide designated CON103, comprising the complete amino acid sequence set forth in SEQ ID NO: 6. This amino acid sequence was deduced from a polynucleotide sequence encoding CON103 (SEQ ID NO: 5), as set forth below:

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      ggggctact tcaccgtgta cccggacttg ggaccatcac agacttcaga accatcagga 60
      acctgggagc aactgaaagc tgaactacag tgggctttca gacacacagc aggctgcgga 120
      gcacaaatag gactgggtcc ctccaggcca ccagcagggc ggtggagggtc ttcactgact 180
25     ccctgcctac ctctcaggac aatgtccttt tgggtccaca gtccctgaag ccagagctgg 240
      tgggggcagg gaggcagcca ccagcctcta tatgtagtgg aggaggggggt gtccagggag 300
      ggctgcatga tcctgagagc cccacactca cccggctgga ctatcctccc acttcagggt 360
      ttctctgggc ttccatcttg cccctgctga gccctgcttc ctctctacc agcagcacia 420
      cccccaggct gggctcagag acctcatgtg gtgggatcac tcagtacccc gaggcggagg 480
30     gaaggaggga gggctgcagg gttccccctg gcctgcaaac aggaacacag ggtgtttctc 540
      agtggctgcg agaatgctga tgaaaacccc aggatgttgt gtcaccgtgg tggccagctg 600
      atagtgccaa tcateccact ttgcctgag cactcctgca ggggtagaag actccagaac 660
      cttctctcag gcccatggcc caagcagccc atg gaa ctt cat aac ctg agc tct 714
                                Met Glu Leu His Asn Leu Ser Ser
35     1                                5
      cca tct ccc tct ctc tcc tcc tct gtt ctc cct ccc tcc ttc tct ccc 762
      Pro Ser Pro Ser Leu Ser Ser Ser Val Leu Pro Pro Ser Phe Ser Pro
                10                15                20
      tca ccc tcc tct gct ccc tct gcc ttt acc act gtg ggg ggg tcc tct 810
40     Ser Pro Ser Ser Ala Pro Ser Ala Phe Thr Thr Val Gly Gly Ser Ser
      25                30                35                40

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- 8 -

gga ggg ccc tgc cac ccc acc tct tcc tcg ctg gtg tct gcc ttc ctg 858
 Gly Gly Pro Cys His Pro Thr Ser Ser Ser Leu Val Ser Ala Phe Leu
 45 50 55
 gca cca atc ctg gcc ctg gag ttt gtc ctg ggc ctg gtg ggg aac agt 906
 5 Ala Pro Ile Leu Ala Leu Glu Phe Val Leu Gly Leu Val Gly Asn Ser
 60 65 70
 ttg gcc ctc ttc atc ttc tgc atc cac acg cgg ccc tgg acc tcc aac 954
 Leu Ala Leu Phe Ile Phe Cys Ile His Thr Arg Pro Trp Thr Ser Asn
 75 80 85
 10 acg gtg ttc ctg gtc agc ctg gtg gcc gct gac ttc ctc ctg atc agc 1002
 Thr Val Phe Leu Val Ser Leu Val Ala Ala Asp Phe Leu Leu Ile Ser
 90 95 100
 aac ctg ccc ctc cgc gtg gac tac tac ctc ctc cat gag acc tgg cgc 1050
 Asn Leu Pro Leu Arg Val Asp Tyr Leu Leu His Glu Thr Trp Arg
 15 105 110 115 120
 ttt ggg gct gct gcc tgc aaa gtc aac ctc ttc atg ctg tcc acc aac 1098
 Phe Gly Ala Ala Ala Cys Lys Val Asn Leu Phe Met Leu Ser Thr Asn
 125 130 135
 cgc acg gcc agc gtt gtc ttc ctc aca gcc atc gca ctc aac cgc tac 1146
 20 Arg Thr Ala Ser Val Val Phe Leu Thr Ala Ile Ala Leu Asn Arg Tyr
 140 145 150
 ctg aag gtg gtg cag ccc cac cac gtg ctg agc cgt gct tcc gtg ggg 1194
 Leu Lys Val Val Gln Pro His His Val Leu Ser Arg Ala Ser Val Gly
 155 160 165
 25 gca gct gcc cgg gtg gcc ggg gga ctc tgg gtg ggc atc ctg ctc ctc 1242
 Ala Ala Ala Arg Val Ala Gly Gly Leu Trp Val Gly Ile Leu Leu Leu
 170 175 180
 aac ggg cac ctg ctc ctg agc acc ttc tcc ggc ccc tcc tgc ctc agc 1290
 Asn Gly His Leu Leu Leu Ser Thr Phe Ser Gly Pro Ser Cys Leu Ser
 30 185 190 195 200
 tac agg gtg ggc acg aag ccc tcg gcc tcg ctc cgc tgg cac cag gca 1338
 Tyr Arg Val Gly Thr Lys Pro Ser Ala Ser Leu Arg Trp His Gln Ala
 205 210 215
 ctg tac ctg ctg gag ttc ttc ctg cca ctg gcg ctc atc ctc ttt gct 1386
 35 Leu Tyr Leu Leu Glu Phe Phe Leu Pro Leu Ala Leu Ile Leu Phe Ala
 220 225 230
 att gtg agc att ggg ctc acc atc cgg aac cgt ggt ctg ggc ggg cag 1434
 Ile Val Ser Ile Gly Leu Thr Ile Arg Asn Arg Gly Leu Gly Gly Gln
 235 240 245
 40 gca ggc ccg cag agg gcc atg cgt gtg ctg gcc atg gtg gtg gcc gtc 1482
 Ala Gly Pro Gln Arg Ala Met Arg Val Leu Ala Met Val Val Ala Val
 250 255 260

- 9 -

tac acc atc tgc ttc ttg ccc agc atc atc ttt ggc atg gct tcc atg 1530
 Tyr Thr Ile Cys Phe Leu Pro Ser Ile Ile Phe Gly Met Ala Ser Met
 265 270 275 280
 gtg gct ttc tgg ctg tcc gcc tgc cga tcc ctg gac ctc tgc aca cag 1578
 5 Val Ala Phe Trp Leu Ser Ala Cys Arg Ser Leu Asp Leu Cys Thr Gln
 285 290 295
 ctc ttc cat ggc tcc ctg gcc ttc acc tac ctc aac agt gtc ctg gac 1626
 Leu Phe His Gly Ser Leu Ala Phe Thr Tyr Leu Asn Ser Val Leu Asp
 300 305 310
 10 ccc gtg ctc tac tgc ttc tct agc ccc aac ttc ctc cac cag agc cgg 1674
 Pro Val Leu Tyr Cys Phe Ser Ser Pro Asn Phe Leu His Gln Ser Arg
 315 320 325
 gcc ttg ctg ggc ctc acg cgg gcc cgg cag ggc cca gtg agc gac gag 1722
 Ala Leu Leu Gly Leu Thr Arg Gly Arg Gln Gly Pro Val Ser Asp Glu
 15 330 335 340
 agc tcc tac caa ccc tcc agg cag tgg cgc tac cgg gag gcc tct agg 1770
 Ser Ser Tyr Gln Pro Ser Arg Gln Trp Arg Tyr Arg Glu Ala Ser Arg
 345 350 355 360
 aag gcg gag gcc ata ggg aag ctg aaa gtg cag ggc gag gtc tct ctg 1818
 20 Lys Ala Glu Ala Ile Gly Lys Leu Lys Val Gln Gly Glu Val Ser Leu
 365 370 375
 gaa aag gaa ggc tcc tcc cag ggc tga gggccagctg cagggtgca 1865
 Glu Lys Glu Gly Ser Ser Gln Gly
 380 385
 25 gcgctgtggg ggtaagggt gccgcgtctt ggcttgagg gacaaggcca gcacacggtg1925
 cctcaaccaa ctggacaagg gatggcgga gaccaggggc caggccaaag cactggcagg1985
 actcatgtgg gtggcaggga gagaaaccca cctaggcctc tcagtgtgtc caggatggca2045
 ttcccagaat gcaggggaga gcaggatgcc ggggtggagga gacaggcaag gtgccgttgg2105
 cacaccagct cagacagggg cctgcgcagc tgcaggggac agacgccaat cactgtcaca2165
 30 gcagagtcac cttagaaatt ggacagctgc atgttctgtg ctctccagtt tgtcccttcc2225
 aatattaata aacttccctt ttaaatatat ttatttgcag accaatatct gtctttaatt2285
 ctaacctggg actgtcagta ggcgtcaaag tgagcgcccc agtgaaggaa ccttggagag2345
 agtgggagca ttcccagcct tccaggggga ctcgctcttcc agactttgga gcccgcagtg2405
 ctgaagcaga ctcttcttg gtag 2429

35 Another preferred embodiment comprises a purified and isolated
 polypeptide designated CON203, comprising the complete amino acid sequence set
 forth in SEQ ID NO: 8. This amino acid sequence was deduced from a
 polynucleotide sequence encoding CON203 (SEQ ID NO: 7), as set forth below:
 40 ttgaatttag gtgacactat agaagagcta tgacgtcgca tgcacgcgta cgtaagctcg 60
 gaattcggct cgagctgaac taatgactgc cgccataaga agacagagag aactgagtat 120

- 10 -

	cctcccaaag gtgacactgg aagca atg aac acc aca gtg atg caa ggc ttc	172
	Met Asn Thr Thr Val Met Gln Gly Phe	
	1 5	
5	aac aga tct gag cgg tgc ccc aga gac act cgg ata gta cag ctg gta	220
	Asn Arg Ser Glu Arg Cys Pro Arg Asp Thr Arg Ile Val Gln Leu Val	
	10 15 20 25	
	ttc cca gcc ctc tac aca gtg gtt ttc ttg acc ggc atc ctg ctg aat	268
	Phe Pro Ala Leu Tyr Thr Val Val Phe Leu Thr Gly Ile Leu Leu Asn	
	30 35 40	
10	act ttg gct ctg tgg gtg ttt gtt cac atc ccc agc tcc tcc acc ttc	316
	Thr Leu Ala Leu Trp Val Phe Val His Ile Pro Ser Ser Ser Thr Phe	
	45 50 55	
	atc atc tac ctc aaa aac act ttg gtg gcc gac ttg ata atg aca ctc	364
	Ile Ile Tyr Leu Lys Asn Thr Leu Val Ala Asp Leu Ile Met Thr Leu	
15	60 65 70	
	atg ctt cct ttc aaa atc ctc tct gac tca cac ctg gca ccc tgg cag	412
	Met Leu Pro Phe Lys Ile Leu Ser Asp Ser His Leu Ala Pro Trp Gln	
	75 80 85	
	ctc aga gct ttt gtg tgt cgt ttt tct tcg gtg ata ttt tat gag acc	460
20	Leu Arg Ala Phe Val Cys Arg Phe Ser Ser Val Ile Phe Tyr Glu Thr	
	90 95 100 105	
	atg tat gtg ggc atc gtg ctg tta ggg ctc ata gcc ttt gac aga ttc	508
	Met Tyr Val Gly Ile Val Leu Leu Gly Leu Ile Ala Phe Asp Arg Phe	
	110 115 120	
25	ctc aag atc atc aga cct ttg aga aat att ttt cta aaa aaa cct gtt	556
	Leu Lys Ile Ile Arg Pro Leu Arg Asn Ile Phe Leu Lys Lys Pro Val	
	125 130 135	
	ttt gca aaa acg gtc tca atc ttc atc tgg gtc ttt ttg gtc ttc atc	604
	Phe Ala Lys Thr Val Ser Ile Phe Ile Trp Val Phe Leu Val Phe Ile	
30	140 145 150	
	tcc ctg cca aat atg atc ttg agc aac aag gaa gca aca cca tcg tct	652
	Ser Leu Pro Asn Met Ile Leu Ser Asn Lys Glu Ala Thr Pro Ser Ser	
	155 160 165	
	gtg aaa aag tgt gct tcc tta aag ggg cct ctg ggg ctg aaa tgg cat	700
35	Val Lys Lys Cys Ala Ser Leu Lys Gly Pro Leu Gly Leu Lys Trp His	
	170 175 180 185	
	caa atg gta aat aac ata tgc cag ttt att ttc tgg act ggt ttt atc	748
	Gln Met Val Asn Asn Ile Cys Gln Phe Ile Phe Trp Thr Gly Phe Ile	
	190 195 200	
40	cta atg ctt gtg ttt tat gtg gtt att gca aaa aaa gta tat gat tct	796
	Leu Met Leu Val Phe Tyr Val Val Ile Ala Lys Lys Val Tyr Asp Ser	
	205 210 215	

- 11 -

tat aga aag tcc aaa agt aag gac aga aaa aac aac aaa aag ctg gaa 844
 Tyr Arg Lys Ser Lys Ser Lys Asp Arg Lys Asn Asn Lys Lys Leu Glu
 220 225 230
 ggc aaa gta ttt gtt gtc gtg gct gtc ttc ttt gtg tgt ttt gct cca 892
 Gly Lys Val Phe Val Val Val Ala Val Phe Phe Val Cys Phe Ala Pro
 235 240 245
 ttt cat ttt gcc aga gtt cca tat act cac agt caa acc aac aat aag 940
 Phe His Phe Ala Arg Val Pro Tyr Thr His Ser Gln Thr Asn Asn Lys
 250 255 260 265
 act gac tgt aga ctg caa aat caa ctg ttt att gct aaa gaa aca act 988
 Thr Asp Cys Arg Leu Gln Asn Gln Leu Phe Ile Ala Lys Glu Thr Thr
 270 275 280
 ctc ttt ttg gca gca act aac att tgt atg gat ccc tta ata tac ata 1036
 Leu Phe Leu Ala Ala Thr Asn Ile Cys Met Asp Pro Leu Ile Tyr Ile
 285 290 295
 ttc tta tgt aaa aaa ttc aca gaa aag cta cca tgt atg caa ggg aga 1084
 Phe Leu Cys Lys Lys Phe Thr Glu Lys Leu Pro Cys Met Gln Gly Arg
 300 305 310
 aag acc aca gca tca agc caa gaa aat cat agc agt cag aca gac aac 1132
 Lys Thr Thr Ala Ser Ser Gln Glu Asn His Ser Ser Gln Thr Asp Asn
 315 320 325
 ata acc tta ggc tga caactgtaca taggggtaac ttctatttat tgatgagact 1187
 Ile Thr Leu Gly
 330
 tccgtagata atgtggaaat caaatttaac caagaaaaaa agattggaac aaatgctctc1247
 ttacatttta tttatcctgg tgtccaggaa aagattatat taaatttaaa tccacataga1307
 tctattcata agctgaatga accattacct aagagaatgc aacaggatac caatggccac1367
 tagaggcata ttccttcttc tttttttttt gttaaatttc aagagcattc actttacatt1427
 tggaaagact aaggggaacg gttatcctac aaacctccct tcaacacctt ttacatt 1484

30 Another preferred embodiment comprises a purified and isolated
 polypeptide designated CON198, comprising the complete amino acid sequence set
 forth in SEQ ID NO: 10. This amino acid sequence was deduced from a
 polynucleotide sequence encoding CON198 (SEQ ID NO: 9), as set forth below:

35 atg atg gtg gat ccc aat ggc aat gaa tcc agt gct aca tac ttc atc 48
 Met Met Val Asp Pro Asn Gly Asn Glu Ser Ser Ala Thr Tyr Phe Ile
 1 5 10 15
 cta ata ggc ctc cct ggt tta gaa gag gct cag ttc tgg ttg gcc ttc 96
 Leu Ile Gly Leu Pro Gly Leu Glu Glu Ala Gln Phe Trp Leu Ala Phe
 20 25 30
 cca ttg tgc tcc ctg tac ctt att gct gtg cta ggt aac ttg aca atc 144
 Pro Leu Cys Ser Leu Tyr Leu Ile Ala Val Leu Gly Asn Leu Thr Ile
 35 40 45

45

- 12 -

	atc	tac	att	gtg	cgg	act	gag	cac	agc	ctg	cat	gag	ccc	atg	tat	ata	192
	Ile	Tyr	Ile	Val	Arg	Thr	Glu	His	Ser	Leu	His	Glu	Pro	Met	Tyr	Ile	
	50						55					60					
5	ttt	ctt	tgc	atg	ctt	tca	ggc	att	gac	atc	ctc	atc	tcc	acc	tca	tcc	240
	Phe	Leu	Cys	Met	Leu	Ser	Gly	Ile	Asp	Ile	Leu	Ile	Ser	Thr	Ser	Ser	
	65					70					75					80	
10	atg	ccc	aaa	atg	ctg	gcc	atc	ttc	tgg	ttc	aat	tcc	act	acc	atc	cag	288
	Met	Pro	Lys	Met	Leu	Ala	Ile	Phe	Trp	Phe	Asn	Ser	Thr	Thr	Ile	Gln	
					85				90						95		
15	ttt	gat	gct	tgt	ctg	cta	cag	atg	ttt	gcc	atc	cac	tcc	tta	tct	ggc	336
	Phe	Asp	Ala	Cys	Leu	Leu	Gln	Met	Phe	Ala	Ile	His	Ser	Leu	Ser	Gly	
				100					105					110			
20	atg	gaa	tcc	aca	gtg	ctg	ctg	gcc	atg	gct	ttt	gac	cgc	tat	gtg	gcc	384
	Met	Glu	Ser	Thr	Val	Leu	Leu	Ala	Met	Ala	Phe	Asp	Arg	Tyr	Val	Ala	
			115					120					125				
25	atc	tgt	cac	cca	ctg	cgc	cat	gcc	aca	gta	ctt	acg	ttg	cct	cgt	gtc	432
	Ile	Cys	His	Pro	Leu	Arg	His	Ala	Thr	Val	Leu	Thr	Leu	Pro	Arg	Val	
	130						135					140					
30	acc	aaa	att	ggt	gtg	gct	gct	gtg	gtg	cgg	ggg	gct	gca	ctg	atg	gca	480
	Thr	Lys	Ile	Gly	Val	Ala	Ala	Val	Val	Arg	Gly	Ala	Ala	Leu	Met	Ala	
	145					150					155					160	
35	ccc	ctt	cct	gtc	ttc	atc	aag	cag	ctg	ccc	ttc	tgc	cgc	tcc	aat	atc	528
	Pro	Leu	Pro	Val	Phe	Ile	Lys	Gln	Leu	Pro	Phe	Cys	Arg	Ser	Asn	Ile	
					165					170					175		
40	ctt	tcc	cat	tcc	tac	tgc	cta	cac	caa	gat	gtc	atg	aag	ctg	gcc	tgt	576
	Leu	Ser	His	Ser	Tyr	Cys	Leu	His	Gln	Asp	Val	Met	Lys	Leu	Ala	Cys	
				180					185					190			
45	gat	gat	atc	cgg	gtc	aat	gtc	gtc	tat	ggc	ctt	atc	gtc	atc	atc	tcc	624
	Asp	Asp	Ile	Arg	Val	Asn	Val	Val	Tyr	Gly	Leu	Ile	Val	Ile	Ile	Ser	
			195					200					205				
50	gcc	att	ggc	ctg	gac	tca	ctt	ctc	atc	tcc	ttc	tca	tat	ctg	ctt	att	672
	Ala	Ile	Gly	Leu	Asp	Ser	Leu	Leu	Ile	Ser	Phe	Ser	Tyr	Leu	Leu	Ile	
		210					215					220					
55	ctt	aag	act	gtg	ttg	ggc	ttg	aca	cgt	gaa	gcc	cag	gcc	aag	gca	ttt	720
	Leu	Lys	Thr	Val	Leu	Gly	Leu	Thr	Arg	Glu	Ala	Gln	Ala	Lys	Ala	Phe	
	225					230					235					240	
60	ggc	act	tgc	gtc	tct	cat	gtg	tgt	gct	gtg	ttc	ata	ttc	tat	gta	cct	768
	Gly	Thr	Cys	Val	Ser	His	Val	Cys	Ala	Val	Phe	Ile	Phe	Tyr	Val	Pro	
				245					250						255		
65	ttc	att	gga	ttg	tcc	atg	gtg	cat	cgc	ttt	agc	aag	cgg	cgt	gac	tct	816
	Phe	Ile	Gly	Leu	Ser	Met	Val	His	Arg	Phe	Ser	Lys	Arg	Arg	Asp	Ser	
				260					265					270			
70	cgg	ctg	ccc	gtc	atc	ttg	gcc	aat	atc	tat	ctg	ctg	gtt	cct	cct	gtg	864
	Pro	Leu	Pro	Val	Ile	Leu	Ala	Asn	Ile	Tyr	Leu	Leu	Val	Pro	Pro	Val	
			275					280					285				
75	ctc	aac	cca	att	gtc	tat	gga	gtg	aag	aca	aag	gag	att	cga	cag	cgc	912
	Leu	Asn	Pro	Ile	Val	Tyr	Gly	Val	Lys	Thr	Lys	Glu	Ile	Arg	Gln	Arg	
		290					295					300					

- 13 -

atc ctt cga ctt ttc cat gtg gcc aca cac gct tca gag ccc tag 957
 Ile Leu Arg Leu Phe His Val Ala Thr His Ala Ser Glu Pro
 305 310 315

It will be appreciated that SEQ ID NO: 10 contains methionine residues at positions 1 and 2. Translation of the relevant mRNA sequences may occur beginning from either or both methionines, which can be determined for a particular cell source by purifying expressed CON198 protein and performing amino-terminal sequencing thereon. CON198 polypeptides beginning at either Met₁ or Met₂ of SEQ ID NO: 10 are intended a polypeptides of the invention.

Another preferred embodiment comprises a purified and isolated polypeptide designated CON197, comprising the complete amino acid sequence set forth in SEQ ID NO: 12. This amino acid sequence was deduced from a polynucleotide sequence encoding CON197 (SEQ ID NO: 11), as set forth below:

1
 15 ATGGAAGCGAGAACAGAAGAGTGATAAGAGAATTCATCCTCCTTGGTCTGACCCAGTCTCAAGATATT
 M E S E N R R V I R E F I L L G L T Q S Q D I

70
 20 CAGCTCCTGGTCTTTGTGCTAGTTTTAATATTCTACTTCATCATCCTCCCTGGAAATTTTCTCATTATT
 Q L L V F V L V L I F Y F I I L P G N F L I I

139
 25 TTCACCATAAAGTCAGACCCTGGGCTCACAGCCCCCTCTATTTCTTTCTGGGCAACTTGGCCTTCCTG
 F T I K S D P G L T A P L Y F F L G N L A F L

208
 30 GATGCATCCTACTCCTTCATTGTGGCTCCCCGGATGTTGGTGGACTTCCTCTCTGCGAAGAAGATAATC
 D A S Y S F I V A P R M L V D F L S A K K I I

277
 35 TCCTACAGAGGCTGCATCACTCAGCTCTTTTCTTGCACTTCCTTGGAGGAGGGGAGGGATTACTCCTT
 S Y R G C I T Q L F F L H F L G G G E G L L L

346
 40 GTTGTGATGGCCTTTGACCGCTACATCGCCATCTGCCGGCCTCTGCACTATCCTACTGTCATGAACCTT
 V V M A F D R Y I A I C R P L H Y P T V M N P

415
 45 AGAACCTGCTATGCAATGATGTTGGCTCTGTGGCTTGGGGGTTTTGTCCACTCCATTATCCAGGTGGTC
 R T C Y A M M L A L W L G G F V H S I I Q V V

484
 50 CTCATCCTCCGCTTGCCCTTTTGTGGCCCAACCAGCTGGACAACCTTCTTCTGTGATGTCCACAGGTC
 L I L R L P F C G P N Q L D N F F C D V P Q V

553
 ATCAAGCTGGCCTGCACCGACACATTTGTGGTGGAGCTTCTGATGGTCTTCAACAGTGGCCTGATGACA
 I K L A C T D T F V V E L L M V F N S G L M T

622
 CTCCTGTGCTTTCTGGGGCTTCTGGCCTCTATGCAGTCATTCTTTGTGCGCATACGAGGGTCTTCTTCT
 L L C F L G L L A S Y A V I L C R I R G S S S

- 14 -

691
GAGGCAAAAAACAAGGCCATGTCCACGTGCATCACCCATATCATTGTTATATTCTTCATGTTGGACCT
E A K N K A M S T C I T H I I V I F F M F G P

5 760
GGCATCTTCATCTACACGCGCCCTTCAGGGCTTTCCAGCTGACAAGGTGGTTTCTCTCTCCACACA
G I F I Y T R P F R A F P A D K V V S L F H T

10 829
GTGATTTTTCCTTTGTTGAATCCTGTCAATTTATACCTTCGCAACCAGGAAGTGAAAGCTTCCATGAAA
V I F P L L N P V I Y T L R N Q E V K A S M K

15 898
AAGGTGTTTAATAAGCACATAGCCTGAAAAAGGGCGCAAAAAAAAAAAGAATAAAAAATAGACTGTAGAA
K V F N K H I A *

967
TTTTTAAAAAAAAAAAAAAAAAAAAAAAAA

Another preferred embodiment comprises a purified and isolated

20 polypeptide designated CON202, comprising the complete amino acid sequence set
forth in SEQ ID NO: 14. This amino acid sequence was deduced from a
polynucleotide sequence encoding CON202 (SEQ ID NO: 13), as set forth below:

1
TGCTTCCCCATAAGGTAACAGCTTTGTTAGCNCCTGTCTGACATCATTGCTTGTNACTTAAGAACTGAT

25 70
AGGTNTTTTTTTTTTTTTTTTTTTTTCAGATATTCTGATGGCAAAACAAGTGAAGAAAAGAGGAAGCATGA

139
CTGCAGATCAGATCAGTTCTCTTTGTGGATTATATTTTCAGTAAATGTATGGATCTATCTTTTCCTTG

30 208
TTCTTATATCTAGATCATGAGACTTGAAGCTGTATCCTTATCCTCCATCCATCTATGGCGAACTA
M A N Y

35 277
TAGCCATGCAGCTGACAACATTTTGCAAAATCTCTCGCCTCTAACAGCCTTTCTGAAACTGACTTCCTT
S H A A D N I L Q N L S P L T A F L K L T S L

40 346
GGGTTTCATAATAGGAGTCAGCGTGGTGGGCAACCTCCTGATCTCCATTTTGCTAGTGAAAGATAAGAC
G F I I G V S V V G N L L I S I L L V K D K T

45 415
CTTGCATAGAGCACCTTACTACTTCTGTTGGATCTTTGCTGTTTCTGATATCCTCAGATCTGCAATTTG
L H R A P Y Y F L L D L C C S D I L R S A I C

50 484
TTTCCCATTTGTGTTCAACTCTGTCAAAAATGGTTCTACCTGGACTTATGGGACTCTGACTTGCAAAGT
F P F V F N S V K N G S T W T Y G T L T C K V

553
GATTGCCTTTCTGGGGGTTTTGTCCTGTTTCCACACTGCTTTTCATGCTCTTCTGCATCAGTGTCACCAG
I A F L G V L S C F H T A F M L F C I S V T R

55 622
ATATTTAGCTATCGCCCATCACCGCTTCTATACAAAGAGGCTGACCTTTTGGACGTGTCTGGCTGTGAT
Y L A I A H H R F Y T K R L T F W T C L A V I

- 15 -

691
CTGTATGGTGTGGACTCTGTCTGTGGCCATGGCATTTCCTCCCGGTTTTAGACGTGGGCACTTACTCATT
C M V W T L S V A M A F P P V L D V G T Y S F

5 760
CATTAGGGAGGAAGATCAATGCACCTTCCAACACCGCTCCTTCAGGGCTAATGATTCCCTAGAATTTAT
I R E E D Q C T F Q H R S F R A N D S L G F M

829
10 GCTGCTTCTTGCTCTCATCCTCCTAGCCACACAGCTTGTCTACCTCAAGCTGATATTTTTCTCCACGA
L L L A L I L L A T Q L V Y L K L I F F V H D

898
15 TCGAAGAAAAATGAAGCCAGTCCAGTTTGTAGCAGCAGTCAGCCAGAACTGGACTTTTCATGGTCTCTGG
R R K M K P V Q F V A A V S Q N W T F H G P G

967
20 AGCCAGTGGCCAGGCAGCTGCCAATTGGCTAGCAGGATTGGAAGGGGTCCACACCACCCACCTTGCT
A S G Q A A A N W L A G F G R G P T P P T L L

1036
25 GGGCATCAGGCAAAATGCAAACACCACAGGCAGAAGAAGGCTATTGGTCTTAGACGAGTTCAAAATGGA
G I R Q N A N T T G R R R L L V L D E F K M E

1105
30 GAAAAGAATCAGCAGAATGTTCTATATAATGACTTTTCTGTTTCTAACCTTGTGGGGCCCTACCTGGT
K R I S R M F Y I M T F L F L T L W G P Y L V

1174
35 GGCCTGTTATTGGAGAGTTTTTGCAAGAGGGCCTGTAGTACCAGGGGGATTCTAACAGCTGCTGTCTG
A C Y W R V F A R G P V V P G G F L T A A V W

1243
40 GATGAGTTTTGCCCAAGCAGGAATCAATCCTTTTGTCTGCATTTTCTCAAACAGGGAGCTGAGGCGCTG
M S F A Q A G I N P F V C I F S N R E L R R C

1312
45 TTTCAGCACAACCCTTCTTTACTGCAGAAAAATCCAGGTTACCAAGGGAACCTTACTGTGTTATATGAGG
F S T T L Y C R K S R L P R E P Y C V I

Still another preferred embodiment comprises a purified and isolated polypeptide designated CON222, comprising the complete amino acid sequence set forth in SEQ ID NO: 16. This amino acid sequence was deduced from a

45 polynucleotide sequence encoding CON222 (SEQ ID NO: 15), as set forth below:

1 ATGTTTAGACCTCTGTGAATCTCTCACATATATTTTAAGAAATCCAGTACTGTGGGTATGCA
M F R P L V N L S H I Y F K K F Q Y C G Y A

67 CCACATGTTTCGCAGCTGTAAACCAAACTGATGGAATTTTCATCTCTAGAGAATCTCTGGCAAGC
P H V R S C K P N T D G I S S L E N L L A S

50 133 ATTATTCAGAGAGTATTTGTCTGGGTTGTATCTGCAGTTACCTGCTTTGGAACATTTTGTGCTT
I I Q R V F V W V V S A V T C F G N I F V I

199 TGCATGCGACCTTATATCAGGTCTGAGAACAAGCTGTATGCCATGTCAATCATTCTCTCTGCTGT
C M R P Y I R S E N K L Y A M S I I S L C C

265 55 GCCGACTGCTTAATGGGAATATATTTATTCGTGATCGGAGGCTTTGACCTAAAGTTTCGTGGAGAA
A D C L M G I Y L F V I G G F D L K F R G E

30 polypeptide designated CON215, comprising the complete amino acid sequence set forth in SEQ ID NO: 18. This amino acid sequence was deduced from a polynucleotide sequence encoding CON215 (SEQ ID NO: 17), as set forth below:

35	atg	ggg	ttc	aac	ttg	acg	ctt	gca	aaa	tta	cca	aat	aac	gag	ctg	cac	48
	Met	Gly	Phe	Asn	Leu	Thr	Leu	Ala	Lys	Leu	Pro	Asn	Asn	Glu	Leu	His	
	1				5					10					15		
40	ggc	caa	gag	agt	cac	aat	tca	ggc	aac	agg	agc	gac	ggg	cca	gga	aag	96
	Gly	Gln	Glu	Ser	His	Asn	Ser	Gly	Asn	Arg	Ser	Asp	Gly	Pro	Gly	Lys	
				20					25					30			
45	aac	acc	acc	ctt	cac	aat	gaa	ttt	gac	aca	att	gtc	ttg	cca	gtg	ctt	144
	Asn	Thr	Thr	Leu	His	Asn	Glu	Phe	Asp	Thr	Ile	Val	Leu	Pro	Val	Leu	
			35					40					45				
45	tat	ctc	att	ata	ttt	gtg	gca	agc	atc	ttg	ctg	aat	ggg	tta	gca	gtg	192
	Tyr	Leu	Ile	Ile	Phe	Val	Ala	Ser	Ile	Leu	Leu	Asn	Gly	Leu	Ala	Val	
		50					55					60					

- 17 -

	tgg atc ttc ttc cac att agg aat aaa acc agc ttc ata ttc tat ctc	240
	Trp Ile Phe Phe His Ile Arg Asn Lys Thr Ser Phe Ile Phe Tyr Leu	
	65 70 75 80	
5	aaa aac ata gtg gtt gca gac ctc ata atg acg ctg aca ttt cca ttt	288
	Lys Asn Ile Val Val Ala Asp Leu Ile Met Thr Leu Thr Phe Pro Phe	
	85 90 95	
10	cga ata gtc cat gat gca gga ttt gga cct tgg tac ttc aag ttt att	336
	Arg Ile Val His Asp Ala Gly Phe Gly Pro Trp Tyr Phe Lys Phe Ile	
	100 105 110	
15	ctc tgc aga tac act tca gtt ttg ttt tat gca aac atg tat act tcc	384
	Leu Cys Arg Tyr Thr Ser Val Leu Phe Tyr Ala Asn Met Tyr Thr Ser	
	115 120 125	
20	atc gtg ttc ctt ggg ctg ata agc att gat cgc tat ctg aag gtg gtc	432
	Ile Val Phe Leu Gly Leu Ile Ser Ile Asp Arg Tyr Leu Lys Val Val	
	130 135 140	
	aag cca ttt ggg gac tct cgg atg tac agc ata acc ttc acg aag gtt	480
	Lys Pro Phe Gly Asp Ser Arg Met Tyr Ser Ile Thr Phe Thr Lys Val	
	145 150 155 160	
25	tta tct gtt tgt gtt tgg gtg atc atg gct gtt ttg tct ttg cca aac	528
	Leu Ser Val Cys Val Trp Val Ile Met Ala Val Leu Ser Leu Pro Asn	
	165 170 175	
30	atc atc ctg aca aat ggt cag cca aca gag gac aat atc cat gac tgc	576
	Ile Ile Leu Thr Asn Gly Gln Pro Thr Glu Asp Asn Ile His Asp Cys	
	180 185 190	
35	tca aaa ctt aaa agt cct ttg ggg gtc aaa tgg cat acg gca gtc acc	624
	Ser Lys Leu Lys Ser Pro Leu Gly Val Lys Trp His Thr Ala Val Thr	
	195 200 205	
40	tat gtg aac agc tgc ttg ttt gtg gcc gtg ctg gtg att ctg atc gga	672
	Tyr Val Asn Ser Cys Leu Phe Val Ala Val Leu Val Ile Leu Ile Gly	
	210 215 220	
	tgt tac ata gcc ata tcc agg tac atc cac aaa tcc agc agg caa ttc	720
	Cys Tyr Ile Ala Ile Ser Arg Tyr Ile His Lys Ser Ser Arg Gln Phe	
	225 230 235 240	
45	ata agt cag tca agc cga aag cga aaa cat aac cag agc atc agg gtt	768
	Ile Ser Gln Ser Ser Arg Lys Arg Lys His Asn Gln Ser Ile Arg Val	
	245 250 255	
50	gtt gtg gct gtg ttt ttt acc tgc ttt cta cca tat cac ttg tgc aga	816
	Val Val Ala Val Phe Phe Thr Cys Phe Leu Pro Tyr His Leu Cys Arg	
	260 265 270	
55	att cct ttt act ttt agt cac tta gac agg ctt tta gat gaa tct gca	864
	Ile Pro Phe Thr Phe Ser His Leu Asp Arg Leu Leu Asp Glu Ser Ala	
	275 280 285	
60	caa aaa atc cta tat tac tgc aaa gaa att aca ctt ttc ttg tct gcg	912
	Gln Lys Ile Leu Tyr Tyr Cys Lys Glu Ile Thr Leu Phe Leu Ser Ala	
	290 295 300	

[illegible]

Another preferred embodiment comprises a purified and isolated polypeptide designated CON217, comprising the complete amino acid sequence set forth in SEQ ID NO: 20. This amino acid sequence was deduced from a polynucleotide sequence encoding CON217 (SEQ ID NO: 19), as set forth below:

20 -41 C ATGGCATCCC CAGCCTAGCT CCCAATCCCA CTTTGGCAGC

1 ATGTTAGCCAACAGCTCCTCAACCAACAGTTCTGTTCTCCCGTGTCTGACTACCGACCTACCCAC
M L A N S S S T N S S V L P C P D Y R P T H

67 CGCCTGCACTTGGTGGTCTACAGCTTGGTGTGGCTGCCGGGCTCCCCCTCAACGCGCTAGCCCTC
R L H L V V Y S L V L A A G L P L N A L A L

25 133 TGGGTCTTCTGCGCGCGCTGCGCGTGCCTCGGTGGTGAAGCTGTACATGTGTAACCTGGCGGCC
W V F L R A L R V H S V V S V Y M C N L A A

199 AGCGACCTGCTCTTACCCTCTCGCTGCCCGTTCTGCTCTCTACTACGCACTGCACCACTGGCCC
S D L L F T L S L P V R L S Y Y A L H H W P

265 TTCCCCGACCTCCTGTGCCAGACGACGGGCGCCATCTTCCAGATGAACATGTACGGCAGCTGCATC
F P D L L C Q T T G A I F Q M N M Y G S C I

30 331 TTCCTGATGCTCATCAACGTGGACCGCTACGCCGCCATCGTGACCCGCTGCGACTGCGCCACCTG
F L M L I N V D R Y A A I V H P L R L R H L

397 CGGCGGCCCCGCGTGGCGCGGCTGCTCTGCCTGGGCGTGTGGGCGCTCATCCTGGTGTGTCGGTG
R R P R V A R L L C L G V W A L I L V F A V

35 463 CCCGCCGCCCGCGTGCACAGGCCCTCGCGTTGCCGCTACCGGGACCTCGAGGTGCGCCTATGCTTC
P A A R V H R P S R C R Y R D L E V R L C F

529 GAGAGCTTCAGCGACGAGCTGTGGAAAGGACGCGTGTGCCCTCGTGCTGCTGGCCGAGGCGCTG
E S F S D E L W K G R L L P L V L L A E A L

595 GGCTTCCTGCTGCCCTTGGCGGCGGTGGTCTACTCGTGGGCGGAGTCTTCTGGACGCTGGCGCGC
G F L L P L A A V V Y S S G R V F W T L A R

40 661 CCCGACGCCACGCAGAGCCAGCGGCGCGGAAGACCGTGCGCTCCTGCTGGCTAACCTCGTCATC
P D A T Q S Q R R R K T V R L L L A N L V I

727 TTCCTGCTGTGCTTCGTGCCCTACAACAGCAGCTGGCGGTCTACGGGCTGCTGCGGAGCAAGCTG
F L L C F V P Y N S T L A V Y G L L R S K L

45 793 GTGGCGGCCAGCGTGCCTGCCCGGATCGCGTGCAGGGGTGCTGATGGTGATGGTGCTGCTGGCC
V A A S V P A R D R V R G V L M V M V L L A

- 19 -

859 GGGGCCAACTGCGTGCTGGACCCGCTGGTGTACTACTTTAGCGCCGAGGGCTTCCGCAACACCCCTG
 G A N C V L D P L V Y Y F S A E G F R N T L
 925 CGCGGCCTGGGCACTCCGCACCGGGCCAGGACCTCGGCCACCAACGGGACGCGGGCGGCTCGCG
 R G L G T P H R A R T S A T N G T R A A L A
 5 991 CAATCCGAAAGGTCCGCCGTACCCACCGACGCCACCAGGCCGATGCCGCCAGTCAGGGGCTGCTC
 Q S E R S A V T T D A T R P D A A S Q G L L
 1057 CGACCCCTCCGACTCCCACTCTCTGTCTTCTTCCACACAGTGTCCCCAGGATTCGCGCCTCTGAACA
 R P S D S H S L S S F T Q C P Q D S A L *
 1123 CACATGCCAT TGCCTGTCC GTGCCGACT CCCAACGCCT CTCGTTCTGG GAGGCTTACA
 10 1183 GGGTGACAC ACAAGAAGGT GGGCTGGGCA CTTGGACCTT TGGGTGGCAA TTCCAGCTTA
 1243 GCAACGCAGA AGAGTACAAA GTGTGGAAGC CAGGGCCCAG GGAAGGCAGT GCTGCTGGAA
 1303 ATGGCTTCTT TAAACTGTGA GCACGCAGAG CACCCCTTCT CCAGCGGTGG GAAGTGATGC
 1363 AGAGAGCCCA CCCGTGCAGA GGCAGAAGA GGACGAAATG CCTTTGGGTG GGCAGGGCAT
 1423 TAAACTGCTA AAAGCTGGTT AGATGGAACA GAAATGGGC ATTCTGGATC TAAACGCCCA
 15 1483 CAGGGGCCCTG AGAGCTGAAG AGCACCAGGT TTGGTGGACA AAGCTACTGA GATGCCTGTT
 1543 CATCTGCTGA CTTCTGTCTA GGCTCATGGA TGCCACCCCC TTTCATTTCG GCCTAGGCTT
 1603 CCCCTGCTCA CCACTGAGGC CTAATACAAG AGTTCCTATG GACAGAACTA CATTCTTTCT
 1663 CGCATAGTGA CTTGTGACAA TTTAGACTTG GCATCCAGCA TGGGATAGTT GGGGCAAGGC
 1723 AAACTAACT TAGAGTTTCC CCCTCAACAA CATCCAAGTC CAAACCCCTT TTAGGTTATC
 20 1783 CTTTCTTCCA TCACATCCCC TTTTCCAGGC CTCCTCCATT TTAGGTCCTT AATATTCTTT
 1843 CTTTTTCTCT CTCTCTCGTT TCTCTTCT CTCTCCTCTC CTCTCCTCTC TCTTCTCTC
 1903 TTCTCTCTCT CTCCTCTCT CTCCTTTGTC CAGAGTAAGG ATAAATTTCT TTCTACTAAA
 1963 GCACTGGTTC TCAAACCTTT TGGTCTCAGA CCCCCTCTT AGAAATTGAG GATCTCAAAG
 2023 AGCTTTGCTT ATATTTTGT CTTTGTATAC TTACCATACT AGAAATTAAA GCGAATACAT
 25 2083 TTTTAAATA AATACACATG CACACATTAC ATTAGCCATG GGAGCAATAA TGTCACCACA
 2143 CACACTTCAT GAAGCCTCTG GAAAACCTA CAGTATACTT GTGAGAGAAT GAGAGTGAAA
 2203 GGGACAAATA ACATCTGTGT AGCAGTATTA TGAAAATAGC TTGACCTGTG GGACTTCCTC
 2263 AGAGGGTTGG TCCCTGGATC AACTTTGAG AACCATACTT GTCCTGAAGT ATTGGAGTTC
 2323 ATGTCTAACT TCTTCCAGG GCATTATGTA CAGTGCTTTT TATTACTGTG GGGAGAGGGC
 30 2383 AGTGCTAAAT AAATTAATCA CTACTGATAA AAAAAAAAAA AAAAAAAAAA AAAAAA

Although SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, and 20 provide
 for particular human sequences, the invention is intended to include within its scope
 other human allelic variants; non-human mammalian forms of GPCR polypeptides,
 and other vertebrate forms of GPCR polypeptides.

It will be appreciated that extracellular epitopes are particularly useful
 for generating and screening for antibodies and other binding compounds that bind to
 receptors such as GPCR polypeptides. Thus, in another preferred embodiment, the
 invention provides a purified and isolated polypeptide comprising at least one
 extracellular domain of a GPCR polypeptide of the invention. By "extracellular
 domain", is it meant the amino terminal extracellular domain or an extracellular loop
 that spans two membrane domains.

- 20 -

A purified and isolated polypeptide comprising the N-terminal extracellular domain of GPCR polypeptides of the invention is highly preferred. Also preferred is a purified and isolated polypeptide comprising a GPCR seven transmembrane receptor fragment selected from the group consisting of the N-terminal extracellular domain of GPCR polypeptides of the invention, transmembrane domains of GPCR polypeptides of the invention, extracellular loops connecting transmembrane domains of GPCR polypeptides of the invention, intracellular loops connecting transmembrane domains of GPCR polypeptides of the invention, the C-terminal cytoplasmic domain of GPCR polypeptides, and fusions thereof. Such fragments may be continuous portions of the native receptor. However, it will also be appreciated that knowledge of the GPCR gene and protein sequences as provided herein permits recombining of various domains that are not contiguous in the native protein.

In another embodiment, the invention provides purified and isolated polynucleotides (*e.g.*, cDNA, genomic DNA, synthetic DNA, RNA, or combinations thereof, single or double stranded) that comprise a nucleotide sequence encoding an amino acid sequence of the polypeptides of the invention. Another embodiment provides a purified and isolated polynucleotide encoding the amino acid sequence of the polypeptide of the invention fused to a heterologous tag amino acid sequence. Such polynucleotides are useful for recombinantly expressing the receptor and also for detecting expression of the receptor in cells (*e.g.*, using Northern hybridization and *in situ* hybridization assays, and Western studies). Polynucleotides encoding polypeptides of the invention also are useful to design antisense and other molecules for the suppression of GPCR polypeptides expression in a cultured cell or animal (for therapeutic purposes or to provide a model for diseases characterized by aberrant GPCR polypeptide expression). Such polynucleotides are also useful to design antisense and other molecules for the suppression of GPCR polypeptide expression in a cultured cell or tissue or in an animal, for therapeutic purposes or to provide a model for diseases characterized by aberrant GPCR polypeptide expression. Specifically excluded from the definition of polynucleotides of the invention are entire isolated chromosomes of native host cells. A preferred polynucleotide set forth in any one of

- 21 -

the SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, and 19 corresponds to a naturally occurring GPCR sequence. It will be appreciated that numerous other sequences exist that also encode GPCR polypeptides having the amino acid sequence set out in SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18 and 20 due to the well-known degeneracy of the universal genetic code. All such sequences represent polynucleotides of the invention.

The invention also provides a purified and isolated polynucleotide comprising a nucleotide sequence that encodes a mammalian seven transmembrane receptor, wherein the polynucleotide hybridizes to a nucleotide sequence set forth in any one of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, or 19 or the non-coding strand complementary thereto, under the following hybridization conditions:

(a) hybridization for 16 hours at 42°C in a hybridization solution comprising 50% formamide, 1% SDS, 1 M NaCl, 10% Dextran sulphate; and

(b) washing 2 times for 30 minutes at 60°C in a wash solution comprising 0.1% SSC, 1% SDS. Polynucleotides that encode a human allelic variant are highly preferred.

A highly preferred polynucleotide of the invention comprises the sequence set forth in SEQ ID NO: 1, which comprises a human CON193 encoding DNA sequence:

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ntggttgttg gaccattaaa atgcattatg gaatttttaa aagttggggg agaggggagac 60
agtaaaaata acctatattt tctcttgttt tttttttttt aactctagga aagcccagac 120
aaattttgag ctatttcata acctaccaga cttatcatgc taactactgaa taaaacagac 180
ctaataccag cttcatttat tctgaatgga gtcccaggac tggaagacac acaactctgg 240
atttccttcc cattctgctc tatgtatggt gtggctatgg tagggaattg tggactcctc 300
tacctcattc actatgagga tgccctgcac aaacccatgt actacttctt ggccatgctt 360
tcctttactg accttggtat gtgctctagt acaatcccta aagccctctg catcttctgg 420
tttcatctca aggacattgg atttgatgaa tgccttgctc agatgttctt catccacacc 480
ttcacaggga tggagtctgg ggtgcttatg cttatggccc tggatcgcta tgtggccatc 540
tgctacccct tacgctattc aactatcctc accaatcctg taattgcaaa ggttgggact 600
gccaccttcc tgagaggggt attactcatt attcccttta ctttcctcac caagcgctg 660
ccctcctgca gaggcaatat acttcccat acctactgtg accacatgtc tgtagccaaa 720
ttgtcctgtg gtaatgtcaa ggtcaatgcc atctatggtc tgatgggtgc cctcctgatt 780
gggggctttg acatactgtg tatcaccatc tcctatacca tgattctccg ggcagtggtc 840
agcctctcct cagcagatgc tcggcagaag gcctttaata cctgcactgc ccacatttgt 900
gccattgttt tctcctatac tccagcttcc ttctccttct tttcccaccg ctttggggaa 960
cacataatcc ccccttcttg ccacatcatt gtagccaata tttatctgct cctaccacc 1020
actatgaacc ctattgtcta tgggggtgaaa accaaacaga tacgagactg tgtcataagg 1080

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- 22 -

atcctttcag gttctaagga taccaaatcc tacagcatgt gaatgaacac ttgccaggag 1140
 tgagaagaga aggaagaat tacttctatt tgccctctat gcaggagttc ataaaaatctt 1200
 tctggaagta ctgtattgat cacaaaatgg agtttgntga ctggtgcatt ctcaataagt 1260
 accttgggaa tctnacatca ctggaaggcc caccacattt ctataaat 1308

5 Also preferred is a polynucleotide comprising nucleotides 157-1119 of
 SEQ ID NO: 1, which represent the portion of SEQ ID NO: 1 that encodes CON193
 amino acids.

Another highly preferred polynucleotide of the invention comprises the
 sequence set forth in SEQ ID NO: 3, which comprises a human CON166 encoding
 10 DNA sequence:

atggatgaaa caggaaatct gacagtatct tctgccacat gccatgacac tattgatgac 60
 ttccgcaatc aagtgtattc caccttgtag tctatgatct ctgttgtagg cttcttttggc 120
 aatggccttg tgctctatgt cctcataaaa acctatcaca agaagtcagc cttcccaagta 180
 tacatgatta atttagcagt agcagatcta ctttgtgtgt gcacactgcc tctccgtgtg 240
 15 gtctattatg ttcacaaagg catttggtct tttggtgact tcttgtgccg cctcagcacc 300
 tatgctttgt atgtcaacct ctattgtagc atcttcttta tgacagccat gagctttttc 360
 cgggtgcattg caattgtttt tccagtccag aacattaatt tggttacaca gaaaaaagcc 420
 aggtttgtgt gtgtaggat ttggattttt gtgattttga ccagttctcc atttctaattg 480
 gccaaaccac aaaaagatga gaaaaataat accaagtgtc ttgagccccc acaagacaat 540
 20 caaactaaaa atcatgtttt ggtcttgcat tatgtgtcat tgtttgttgg ctttatcatc 600
 ccttttgtaa ttataattgt ctgttacaca atgatcattt tgaccttact aaaaaatca 660
 atgaaaaaaa atctgtcaag tcataaaaag gctataggaa tgatcatggt cgtgaccgct 720
 gccttttttag tcagtttcat gccatatcat attcaacgta ccattcacct tcatttttta 780
 cacaatgaaa ctaaaccttg tgattctgtc cttagaatgc agaagtccgt ggtcataacc 840
 25 ttgtctcttg ctgcatccaa ttgttgtttt gacctctccc tatatttctt ttctgggggt 900
 aactttagga aaaggctgtc tacattttag aagcattctt tgtccagcgt gacttatgta 960
 ccagaaaga aggcctcttt gccagaaaaa ggagaagaaa tatgtaaagt atag 1014

The final three nucleotides of this sequence represent a stop codon.

30 Still another highly preferred polynucleotide of the invention
 comprises the sequence set forth in SEQ ID NO: 5, which comprises a human
 CON103 encoding DNA sequence:

ggggcctact tcaccgtgta cccggacttg ggaccatcac agacttcaga accatcagga 60
 acctgggagc aactgaaagc tgaactacag tgggctttca gacacacagc aggctgcgga 120
 gcacaaatag gactggttcc ctccaggcca ccagcagggc ggtggaggtc ttcactgact 180
 35 ccctgcctac ctctcaggac aatgtccttt tggtccaca gtcctgaag ccagagctgg 240
 tgggggcagg gaggcagcca ccagcctcta tatgtagtgg aggagggggt gtccagggag 300
 ggctgcatga tctgagagc ccccactca cccggctgga ctatcctccc acttcagggt 360
 ttctctgggc ttccatcttg cccctgctga gcctgcttc ctctctacc agcagcacia 420
 cccccaggct gggctcagag acctcatgtg tggggatcac tcagtacccc gaggcggagg 480
 40 gaaggaggga gggctgcagg gttcccttg gcctgcaaac aggaacacag ggtgtttctc 540
 agtggctgcg agaattgtga tgaatacccc aggatgttgt gtcaccgtgg tggccagctg 600
 atagtgccaa tcatcccact ttgccttgag cactctgca ggggtagaag actccagaac 660

- 23 -

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cttctctcag gcccatggcc caagcagccc atg gaa ctt cat aac ctg agc tct 714
cca tct ccc tct ctg tcc tcc tct gtt ctg cct ccc tcc ttc tct ccc 762
tca ccc tcc tct gct ccc tct gcc ttt acc act gtg ggg ggg tcc tct 810
gga ggg ccc tgc cac ccc acc tct tcc tgg ctg gtg tct gcc ttc ctg 858
5 gca cca atc ctg gcc ctg gag ttt gtc ctg ggc ctg gtg ggg aac agt 906
ttg gcc ctg ttc atc ttc tgc atc cac acg cgg ccc tgg acc tcc aac 954
acg gtg ttc ctg gtc agc ctg gtg gcc gct gac ttc ctg ctg atc agc 1002
aac ctg ccc ctg cgc gtg gac tac tac ctg ctg cat gag acc tgg cgc 1050
ttt ggg gct gct gcc tgc aaa gtc aac ctg ttc atg ctg tcc acc aac 1098
10 cgc acg gcc agc gtt gtc ttc ctg aca gcc atc gca ctg aac cgc tac 1146
ctg aag gtg gtg cag ccc cac cac gtg ctg agc cgt gct tcc gtg ggg 1194
gca gct gcc cgg gtg gcc ggg gga ctg tgg gtg ggc atc ctg ctg ctg 1242
aac ggg cac ctg ctg ctg agc acc ttc tcc ggc ccc tcc tgc ctg agc 1290
tac agg gtg ggc acg aag ccc tgg gcc tgg ctg cgc tgg cac cag gca 1338
15 ctg tac ctg ctg gag ttc ttc ctg cca ctg gcg ctg atc ctg ttt gct 1386
att gtg agc att ggg ctg acc atc cgg aac cgt ggt ctg ggc ggg cag 1434
gca ggc ccg cag agg gcc atg cgt gtg ctg gcc atg gtg gtg gcc gtc 1482
tac acc atc tgc ttc ttg ccc agc atc atc ttt ggc atg gct tcc atg 1530
gtg gct ttc tgg ctg tcc gcc tgc cga tcc ctg gac ctg tgc aca cag 1578
20 ctg ttc cat ggc tcc ctg gcc ttc acc tac ctg aac agt gtc ctg gac 1626
ccc gtg ctg tac tgc ttc tct agc ccc aac ttc ctg cac cag agc cgg 1674
gcc ttg ctg ggc ctg acg cgg ggc cgg cag ggc cca gtg agc gac gag 1722
agc tcc tac caa ccc tcc agg cag tgg cgc tac cgg gag gcc tct agg 1770
aag gcg gag gcc ata ggg aag ctg aaa gtg cag ggc gag gtc tct ctg 1818
25 gaa aag gaa ggc tcc tcc cag ggc tga gggccagctg cagggctgca 1865
gcgctgtggg ggtaagggct gccgcgctct ggccctggagg gacaaggcca gcacacgggtg 1925
cctcaaccaa ctggacaagg gatggcggga gaccaggggc caggccaaag cactggcagg 1985
actcatgtgg gtggcaggga gagaaaccca cctaggcctc tcagtgtgtc caggatggca 2045
ttcccagaat gcaggggaga gcaggatgcc ggggtggagga gacaggcaag gtgccgttgg 2105
30 cacaccagct cagacagggg cctgcgcagc tgcaggggac agacgccaat cactgtcaca 2165
gcagagtcac cttagaaatt ggacagctgc atgttctgtg ctctccagtt tgtcccttcc 2225
aatattaata aacttccctt ttaaatatat ttatttgcag accaatatct gtctttaatt 2285
ctaacctggg actgtcagta ggcgtcaaag tgagcgcccc agtgaaggaa ccttggagag 2345
agtgggagca ttcccagcct tccaggggga ctgctcttcc agactttgga gcccgcagtc 2405
35 ctgaagcaga ctctttcttg gtag 2429

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Also preferred is a polynucleotide comprising nucleotides 691-1842 of SEQ ID NO:

5, which represent the portion of SEQ ID NO: 5 that encodes CON103 amino acids.

Nucleotides 1843-1845 represent a stop codon.

Another highly preferred polynucleotide of the invention comprises the
 40 sequence set forth in SEQ ID NO: 7, which comprises a CON203-encoding DNA
 sequence:

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ttgaatttag gtgacactat agaagagcta tgacgtcgca tgcacgcgta cgtaagctcg 60
gaattcggct cgagctgaac taatgactgc cgccataaga agacagagag aactgagtat 120
cctcccaaag gtgacactgg aagcaatgaa caccacagtg atgcaaggct tcaacagatc 180

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- 24 -

5 tgagcgggtgc cccagagaca ctcggatagt acagctggta ttcccagccc tctacacagt 240
 ggttttctttg accggcatcc tgctgaatac ttggctctg tgggtgtttg ttcacatccc 300
 cagtcctccc accttcatca tctacctcaa aaacactttg gtggccgact tgataatgac 360
 actcatgctt cctttcaaaa tcctctctga ctcacacctg gcacctggc agctcagagc 420
 10 ttttgtgtgt cgtttttctt cgggtgatatt ttatgagacc atgtatgtgg gcacgtgtgt 480
 gttagggctc atagcctttg acagattcct caagatcacc agacctttga gaaatatttt 540
 tctaaaaaaa cctgtttttg caaaaacggc ctcaatcttc atctgggtct ttttggctct 600
 catctccctg ccaaatatga tcttgagcaa caaggaagca acaccatcgt ctgtgaaaaa 660
 gtgtgcttcc ttaaaggggc ctctggggct gaaatggcat caaatggtaa ataacatatg 720
 15 ccagtttatt ttctggactg gttttatcct aatgcttgtg ttttatgtgg ttattgcaaa 780
 aaaagtatat gattcttata gaaagtcaa aagtaaggac agaaaaaca acaaaaagct 840
 ggaaggcaaa gtatttgttg tcgtggctgt cttctttgtg tgttttgctc catttcattt 900
 tgccagagtt ccatatactc acagtcaaac caacaataag actgactgta gactgcaaaa 960
 tcaactgttt attgctaaag aaacaactct ctttttggca gcaactaaca ttgtatgga 1020
 15 tcctttaata tacatattct tatgtaaaaa attcacagaa aagctaccat gtatgcaagg 1080
 gagaaagacc acagcatcaa gccaagaaaa tcatagcagt cagacagaca acataacctt 1140
 aggctgacaa ctgtacatag ggttaacttc tatttatgta tgagacttcc gtagataatg 1200
 tggaatcaa atttaaccaa gaaaaaaga ttggaacaaa tgctctctta cattttattt 1260
 atcctggtgt ccaggaaaag attatattaa atttaaacc acatagatct attcataagc 1320
 20 tgaatgaacc attacctaag agaatgcaac aggataccaa tggccactag aggcatttc 1380
 cttctctctt ttttttgtt aaatttcaag agcattcact ttacatttgg aaagactaag 1440
 gggaacggtt atcctacaaa cctcccttca acacctttta catt 1484

Also preferred is a polynucleotide comprising nucleotides 146-1144 of SEQ ID NO:

7, which represent the portion of SEQ ID NO: 7 that encodes CON203 amino acids.

25 Nucleotides 1145-1147 represent a stop codon.

Another highly preferred polynucleotide of the invention comprises the sequence set forth in SEQ ID NO: 9, which comprises a human CON198 encoding DNA sequence:

30 ATGATGGTGG ATCCCAATGG CAATGAATCC AGTGCTACAT ACTTCATCCT AATAGGCCTC 60
 CCTGGTTTAG AAGAGGCTCA GTTCTGGTTG GCCTTCCCAT TGTGCTCCCT CTACCTTATT 120
 GCTGTGCTAG GTAACCTGAC AATCATCTAC ATTGTGCGGA CTGAGCACAG CCTGCATGAG 180
 CCCATGTATA TATTTCTTTG CATGCTTTCA GGCATTGACA TCCTCATCTC CACCTCATCC 240
 ATGCCCAAAA TGCTGGCCAT CTTCTGGTTC AATTCCACTA CCATCCAGTT TGATGCTTGT 300
 35 CTGCTACAGA TGTTTGCCAT CCACTCCTTA TCTGGCATGG AATCCACAGT GCTGCTGGCC 360
 ATGGCTTTTG ACCGCTATGT GGCCATCTGT CACCCACTGC GCCATGCCAC AGTACTTACG 420
 TTGCCTCGTG TCACCAAAAT TGGTGTGGCT GCTGTGGTGC GGGGGGCTGC ACTGATGGCA 480
 CCCCCTCCTG TCTTCATCAA GCAGTGCCC TTCTGCCGCT CCAATATCCT TTCCCATTC 540
 TACTGCCCTAC ACCAAGATGT CATGAAGCTG GCCTGTGATG ATATCCGGGT CAATGTCGTC 600
 TATGGCCTTA TCGTCATCAT CTCCGCCATT GGCCTGGACT CACTTCTCAT CTCCTTCTCA 660
 40 TATCTGCTTA TTCTTAAGAC TGTGTTGGGC TTGACACGTG AAGCCCAGGC CAAGGCATTT 720
 GGCACTGCG TCTCTCATGT GTGTGCTGTG TTCATATTCT ATGTACCTTT CATTGGATTG 780
 TCCATGGTGC ATCGCTTTAG CAAGCGCGCT GACTCTCCGC TGCCCGTCAT CTTGGCCAAT 840
 ATCTATCTGC TGGTTCCTCC TGTGCTCAAC CCAATTGTCT ATGGAGTGAA GACAAAGGAG 900
 ATTCGACAGC GCATCCTTCG ACTTTTCCAT GTGGCCACAC ACGCTTCAGA GCCCTAG 957

- 25 -

The last three nucleotides of this sequence represent a stop codon.

Still another A highly preferred polynucleotide of the invention comprises the sequence set forth in SEQ ID NO: 11, which comprises a human CON197 encoding DNA sequence:

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5   ATGGAAGCG AGAACAGAAG AGTGATAAGA GAATTCATCC TCCTTGGTCT GACCCAGTCT 60
   CAAGATATTC AGCTCCTGGT CTTTGTGCTA GTTTTAATAT TCTACTTCAT CATCCTCCCT 120
   GGAAATTTTC TCATTATTTT CACCATAAAG TCAGACCCTG GGCTCACAGC CCCCCTCTAT 180
   TTCTTTCTGG GCAACTTGGC CTTCTGGAT GCATCCTACT CCTTCATTGT GGCTCCCCGG 240
   ATGTTGGTGG ACTTCCTCTC TGCGAAGAAG ATAATCTCCT ACAGAGGCTG CATCACTCAG 300
10  CTCTTTTCT TGCACCTCCT TGGAGGAGGG GAGGGATTAC TCCTTGTGTG GATGGCCTTT 360
   GACCGCTACA TCGCCATCTG CCGGCCTCTG CACTATCCTA CTGTCATGAA CCCTAGAACC 420
   TGCTATGCAA TGATGTTGGC TCTGTGGCTT GGGGGTTTTG TCCACTCCAT TATCCAGGTG 480
   GTCCTCATCC TCCGCTTGCC TTTTGTGGC CCAAACCAGC TGGACAACCT CTTCTGTGAT 540
   GTCCACAGG TCATCAAGCT GGCCTGCACC GACACATTG TGGTGGAGCT TCTGATGGTC 600
15  TTCAACAGTG GCCTGATGAC ACTCCTGTGC TTTCTGGGGC TTCTGGCCTC CTATGCAGTC 660
   ATTCTTTGTC GCATACGAGG GTCTTCTTCT GAGGCAAAAA ACAAGGCCAT GTCCACGTGC 720
   ATCACCCATA TCATTGTTAT ATTCTTCATG TTTGGACCTG GCATCTTCAT CTACACGCGC 780
   CCCTTCAGGG CTTTCCAGC TGACAAGGTG GTTTCTCTCT TCCACACAGT GATTTTTCTT 840
   TTGTTGAATC CTGTCATTA TACCCTTCGC AACCAGGAAG TGAAAGCTTC CATGAAAAAG 900
20  GTGTTTAATA AGCACATAGC CTGA 924

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The last three nucleotides of this sequence represent a stop codon.

Another highly preferred polynucleotide of the invention comprises the sequence set forth in SEQ ID NO: 13, which comprises a human CON202 encoding DNA sequence:

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25  1   TGCTTCCCCA TAAGGTAACA GCTTTGTTAG CNCTGTCTGA CATCATTGCT
   51   TGTWACTTA AGAACTGATA GGTYYYYTTT TTTTYYYYTT TTCAGATATT
   101  CTGATGGCAA AACAAGTGA AGAAAAGAGG AAGCATGACT GCAGATCAGA
   151  TCAGTTCTCT TTGTGGATTA TATTTTCAGT AAAATGTATG GATCTATCTT
   201  TTCCTTGTTT TTATATCTAG ATCATGAGAC TTGACTGAGG CTGTATCCTT
30  251  ATCCTCCATC CATCTATGGC GAACTATAGC CATGCAGCTG ACAACATTTT
   301  GCAAAATCTC TCGCCTCTAA CAGCCTTTCT GAACTGACT TCCTTGGGTT
   351  TCATAATAGG AGTCAGCGTG GTGGGCAACC TCCTGATCTC CATTTTGCTA
   401  GTGAAAGATA AGACCTTGCA TAGAGCACCT TACTACTTCC TGTGGATCT
   451  TTGCTGTTCA GATATCCTCA GATCTGCAAT TTGTTTCCA TTTGTGTTCA
35  501  ACTCTGTCAA AAATGGTTCT ACCTGGACTT ATGGGACTCT GACTTGCAAA
   551  GTGATTGCCT TTCTGGGGGT TTTGTCCTGT TTCCACACTG CTTTCATGCT
   601  CTTCTGCATC AGTGTCACCA GATATTTAGC TATCGCCAT CACCGCTTCT
   651  ATACAAAGAG GCTGACCTTT TGGACGTGTC TGGCTGTGAT CTGTATGGTG
   701  TGGACTCTGT CTGTGGCCAT GGCATTTCCC CCGGTTTTAG ACGTGGGCAC

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- 26 -

751 T T A C T C A T T C A T T A G G G A G G A A G A T C A A T G C A C C T T C C A A C A C C G C T C C T
 801 T C A G G G C T A A T G A T T C C T T A G G A T T T A T G C T G C T T C T T G C T C T A T C C T C
 851 C T A G C C A C A C A G C T T G T C T A C C T C A A G C T G A T A T T T T T C G T C C A C G A T C G
 901 A A G A A A A A T G A A G C C A G T C C A G T T T G T A G C A G C A G T C A G C C A G A A C T G G A
 5 951 C T T T T C A T G G T C C T G G A G C C A G T G G C C A G G C A G C T G C C A A T T G G C T A G C A
 1001 G G A T T T G G A A G G G T C C C A C A C C A C C A C C T T G C T G G G C A T C A G G C A A A A
 1051 T G C A A A C A C C A C A G G C A G A A G A A G G C T A T T G G T C T T A G A C G A G T T C A A A A
 1101 T G G A G A A A A G A A T C A G C A G A A T G T T C T A T A T A A T G A C T T T T C T G T T T C T A
 1151 A C C T T G T G G G G C C C T A C C T G G T G G C C T G T T A T T G G A G A G T T T T T G C A A G
 10 1201 A G G G C C T G T A G T A C C A G G G G A T T T C T A A C A G C T G C T G T C T G G A T G A G T T
 1251 T T G C C C A A G C A G G A A T C A A T C C T T T T G T C T G C A T T T T C T C A A C A G G G A G
 1301 C T G A G G C G C T G T T T C A G C A C A A C C C T T C T T A C T G C A G A A A A T C C A G G T T
 1351 A C C A A G G G A A C C T T A C T G T G T T A T A T G A G G

Also preferred is a polynucleotide comprising nucleotides 266-1375 of SEQ ID NO:

15 13, which represent the portion of SEQ ID NO: 13 that encodes CON202 amino acids.
 Nucleotides 1376-1378 represent a stop codon.

Another highly preferred polynucleotide of the invention comprises the
 sequence set forth in SEQ ID NO: 15, which comprises a human CON222 encoding
 DNA sequence:

20 1 A T G T T T A G A C C T C T T G T G A A T C T C T C T C A C A T A T A T T T T A A G A A A T T C C A
 51 G T A C T G T G G G T A T G C A C C A C A T G T T C G C A G C T G T A A A C C A A A C A C T G A T G
 101 G A A T T T C A T C T C T A G A G A A T C T C T T G G C A A G C A T T A T T C A G A G A T A T T T
 151 G T C T G G G T T G T A T C T G C A G T A C C T G C T T T G G A A C A T T T T T G T C A T T T G
 201 G A T G C G A C C T T A T A T C A G G T C T G A G A A C A A G C T G T A T G C C A T G T C A A T C A
 25 251 T T T C T C T C T G C T G T G C C G A C T G C T T A A T G G A A T A T A T T T A T T C G T G A T C
 301 G G A G G C T T T G A C C T A A A G T T T C G T G G A G A A T A C A A T A A G C A T G C G C A G C T
 351 G T G G A T G G A G A G T A C T C A T T G T C A G C T T G T A G G A T C T T T G C C A T T C T G T
 401 C C A C A G A A G T A T C A G T T T T A C T G T T A A C A T T C T G A C A T T G G A A A A A T A C
 451 A T C T G C A T T G T C T A T C C T T T T A G A T G T G T G A G A C C T G G A A A A T G C A G A A C
 30 501 A A T T A C A G T T C T G A T T C T C A T T T G G A T T A C T G G T T T T A T A G T G G C T T T C A
 551 T T C C A T T G A G C A A T A A G G A A T T T T T C A A A A A C T A C T A T G G C A C C A A T G G A
 601 G T A T G C T T C C C T C T T C A T T C A G A A G A T A C A G A A G T A T T G G A G C C C A G A T
 651 T T A T T C A G T G C A A T T T T T C T T G G T A T T A A T T T G G C C G C A T T T A T C A T C A
 701 T A G T T T T T T C C T A T G G A A G C A T G T T T T A T A G T G T T C A T C A A A G T G C C A T A
 35 751 A C A G C A A C T G A A A T A C G G A A T C A A G T T A A A A A G A G A T G A T C C T T G C C A A
 801 A C G T T T T T T C T T A T A G T A T T A C T G A T G C A T T A T G C T G G A T A C C A T T
 851 T T G T A G T G A A A T T C T T T C A C T G C T T C A G G T A G A A A T A C C A G G T A C C A T A
 901 A C C T C T T G G G T A G T G A T T T T A T T C T G C C C A T T A A C A G T G C T T T G A A C C C
 951 A A T T C T C T A T A C T C T G A C C A C A A G A C C A T T T A A G A A A T G A T T C A T C G G T
 40 1001 T T T G G T A T A A C T A C A G A C A A A G A A A T C T A T G G A C A G C A A A G G T C A G A A A
 1051 A C A T A T G C T C C A T C A T T C A T C T G G G T G G A A A T G T G G C C A C T G C A G G A G A T
 1101 G C C A C C T G A G T T A A T G A A G C C G G A C C T T T T C A C A T A C C C C T G T G A A A T G T

- 27 -

1151 CACTGATTTC TCAATCAACG AGACTCAATT CCTATTCA

The last three nucleotides of this sequence represent a stop codon.

Another highly preferred polynucleotide of the invention comprises the sequence set forth in SEQ ID NO: 17, which comprises a human CON215 encoding DNA sequence. Also preferred is a polynucleotide comprising the portion of SEQ ID NO: 17 set forth below, which represent the portion of SEQ ID NO: 17 that encodes CON215 amino acids (the last three nucleotides represent a stop codon).

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10 ATGGGGTTCA ACTTGACGCT TGCAAAATTA CCAAATAACG AGCTGCACGG CCAAGAGAGT   60
   CACAATTCAG GCAACAGGAG CGACGGGCCA GGAAAGAACA CCACCCTTCA CAATGAATTT   120
   GACACAATTG TCTTGCCAGT GCTTTATCTC ATTATATTTG TGGCAAGCAT CTTGCTGAAT   180
   GGTTTAGCAG TGTGGATCTT CTTCCACATT AGGAATAAAA CCAGCTTCAT ATTCTATCTC   240
   AAAACATAG TGGTTGCAGA CCTCATAATG ACGCTGACAT TTCCATTTTC AATAGTCCAT   300
   GATGCAGGAT TTGGACCTTG GTACTTCAAG TTTATTCTCT GCAGATACAC TTCAGTTTTG   360
   TTTTATGCAA ACATGTATAC TTCCATCGTG TTCCTTGGGC TGATAAGCAT TGATCGCTAT   420
15 CTGAAGGTGG TCAAGCCATT TGGGGACTCT CGGATGTACA GCATAACCTT CACGAAGGTT   480
   TTATCTGTTT GTGTTTGGGT GATCATGGCT GTTTGTCTT TGCCAAACAT CATCCTGACA   540
   AATGGTCAGC CAACAGAGGA CAATATCCAT GACTGCTCAA AACTTAAAG TCCTTTGGGG   600
   GTCAAATGGC ATACGGCAGT CACCTATGTG AACAGCTGCT TGTTTGTGGC CGTGCTGGTG   660
   ATTCTGATCG GATGTTACAT AGCCATATCC AGGTACATCC ACAAATCCAG CAGGCAATTC   720
20 ATAAGTCAGT CAAGCCGAAA GCGAAAACAT AACCAGAGCA TCAGGGTTGT TGTGGCTGTG   780
   TTTTTCACCT GCTTTCTACC ATATCACTTG TGCAGAATTC CTTTACTTT TAGTCACTTA   840
   GACAGGCTTT TAGATGAATC TGCACAAAAA ATCCTATATT ACTGCAAAGA AATTACACTT   900
   TTCTTGCTCG CGTGTAATGT TTGCCTGGAT CCAATAATTT ACTTTTCAT GTGTAGGTCA   960
   TTTTCAAGAA GGCTGTTCAA AAAATCAAAT ATCAGAACCA GGAGTGAAAG CATCAGATCA 1020
25 CTGCAAAGTG TGAGAAGATC GGAAGTTCTC ATATATTATG ATTATACTGA TGTGTAG   1077

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Another preferred polynucleotide of the invention comprises the portion of the sequence set forth in SEQ ID NO: 19 which comprises a human CON217 encoding DNA sequence:

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30 1 ATGTTAGCCA ACAGTCCTC AACCAACAGT TCTGTTCTCC CGTGCCTGA CTACCGACCT
   61 ACCCACC GCC TGCAC TTGGT GGTCTACAGC TTGGTGCTGG CTGCCGGGCT CCCCTCAAC
121 GCGCTAGCCC TCTGGTCTT CCTGCGCGCG CTGCGCGTGC ACTCGGTGGT GAGCGGTAC
181 ATGTGTAACC TGGCGGCCAG CGACCTGCTC TTCACCCTCT CGCTGCCCCG TCGTCTCTCC
241 TACTACGCAC TGCACCACTG GCCCTTCCCC GACCTCCTGT GCCAGACGAC GGGCGCCATC
301 TTCCAGATGA ACATGTACGG CAGCTGCATC TTCCTGATGC TCATCAACGT GGACCGCTAC
35 361 GCCGCCATCG TGCACCCGCT GCGACTGCGC CACCTGCGGC GGCCCCGCGT GGCGCGGCTG
   421 CTCTGCCCTGG GCGTGTGGGC GCTCATCTG GTGTTTGCCG TGCCCGCCGC CCGCGTGCAC
481 AGGCCCTCGC GTTGCCGCTA CCGGACCTC GAGGTGCGCC TATGCTTCGA GAGCTTCAGC
541 GACGAGCTGT GGAAAGGCAG GCTGCTGCCC CTCGTGCTGC TGGCCGAGGC GCTGGGCTTC
601 CTGCTGCCCC TGCGGGCGGT GGTCTACTCG TCGGGCCGAG TCTTCTGGAC GCTGGCGCGC
40 661 CCCGACGCCA CGCAGAGCCA GCGGCGCGG AAGACCGTGC GCCTCCTGCT GGCTAACCTC
   721 GTCATCTTCC TGCTGTGCTT CGTGCCCTAC AACAGCACGC TGGCGGTCTA CGGGCTGCTG
781 CGGAGCAAGC TGGTGGCGGC CAGCGTGCCT GCCCGGATC GCGTGC GCGG GGTGCTGATG

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- 28 -

841 GTGATGGTGC TGCTGGCCGG CGCCAACTGC GTGCTGGACC CGCTGGTGTA CTACTTTAGC
901 GCCGAGGGCT TCCGCAACAC CCTGCGCGGC CTGGGCACTC CGCACCAGGC CAGGACCTCG
961 GCCACCAACG GGACGCGGGC GGCGCTCGCG CAATCCGAAA GGTCCGCCGT CACCACCGAC
1021 GCCACCAGGC CGGATGCCGC CAGTCAGGGG CTGCTCCGAC CCTCCGACTC CCACTCTCTG
5 1081 TCTTCCTTCA CACAGTGTCC CCAGGATTCC GCCCTCTGA

The last three nucleotides of this sequence represent a stop codon.

The invention also includes polynucleotides differing from the sequences set forth in SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17 and 19 and from their complementary strand by at least one nucleotide.

10 In a related embodiment, the invention provides vectors comprising a polynucleotide of the invention. Such vectors are useful, *e.g.*, for amplifying the polynucleotides in host cells to create useful quantities thereof. In preferred embodiments, the vector is an expression vector wherein the polynucleotide of the invention is operatively linked to a polynucleotide comprising an expression control
15 sequence. Such vectors are useful for recombinant production of polypeptides of the invention.

In another related embodiment, the invention provides host cells that are transformed or transfected (stably or transiently) with a polynucleotide of the invention or vectors of the invention. As stated above, such host cells are useful for
20 amplifying the polynucleotides and also for expressing the GPCR seven transmembrane receptor polypeptides or fragments thereof encoded by the polynucleotides. Such host cells are useful in assays as described herein.

In still another related embodiment, the invention provides a method for producing a seven transmembrane receptor polypeptide (or fragment thereof) of
25 the invention comprising the steps of growing a host cell of the invention in a nutrient medium and isolating the polypeptide or variant thereof from the cell or the medium. Since the GPCR polypeptides are seven transmembrane receptors, it will be appreciated that, for some applications, such as certain activity assays, the preferable isolation may involve isolation of cell membranes containing the polypeptide
30 embedded therein, whereas for other applications a more complete isolation may be preferable.

In still another embodiment, the invention provides antibodies that are specific for the GPCR seven transmembrane receptors of the invention. Antibody

- 29 -

specificity is described in greater detail below. However, it should be emphasized that antibodies that can be generated from polypeptides that have previously been described in the literature and that are capable of fortuitously cross-reacting with the GPCR polypeptides of the invention (e.g., due to the fortuitous existence of a similar epitope in both polypeptides) are considered "cross-reactive" antibodies. Such cross-reactive antibodies are not antibodies that are "specific" for the GPCR polypeptides. The determination of whether an antibody is specific for a GPCR polypeptide or is cross-reactive with another known receptor is made using Western blotting assays or several other assays well known in the literature. For identifying cells that express GPCR polypeptides and also for modulating GPCR -ligand binding activity, antibodies that specifically bind to an extracellular epitope of one of the GPCR seven transmembrane receptors of the present invention are preferred.

In one preferred variation, the invention provides monoclonal antibodies. Hybridomas that produce such antibodies also are intended as aspects of the invention. In yet another variation, the invention provides a humanized antibody. Humanized antibodies are useful for *in vivo* therapeutic indications.

In another variation, the invention provides a cell-free composition comprising polyclonal antibodies, wherein at least one of the antibodies is an antibody of the invention specific for a GPCR polypeptide of the present invention. Antisera isolated from an animal is an exemplary composition, as is a composition comprising an antibody fraction of an antisera that has been resuspended in water or in another diluent, excipient, or carrier.

In still another related embodiment, the invention provides anti-idiotypic antibodies specific for an antibody that is specific for a GPCR polypeptide of the present invention.

It is well known that antibodies contain relatively small antigen binding domains that can be isolated chemically or by recombinant techniques. Such domains are useful GPCR binding molecules themselves, and also may be reintroduced into human antibodies, or fused to toxins or other polypeptides. Thus, in still another embodiment, the invention provides a polypeptide comprising a fragment of a GPCR-specific antibody, wherein the fragment and the polypeptide bind to a

- 30 -

GPCR seven transmembrane receptor of the present invention. By way of non-limiting example, the invention provides polypeptides that are single chain antibodies and CDR-grafted antibodies.

5 Also within the scope of the invention are compositions comprising polypeptides, polynucleotides, or antibodies of the invention that have been formulated with, *e.g.*, a pharmaceutically acceptable carrier.

The invention also provides methods of using antibodies of the invention. For example, the invention provides a method for modulating ligand binding of a GPCR seven transmembrane receptor of the present invention comprising
10 the step of contacting the seven transmembrane receptor with an antibody specific for the seven transmembrane receptor, under conditions wherein the antibody binds the receptor.

GPCR polypeptides are expressed in the brain, providing an indication that aberrant GPCR polypeptide signaling activity may correlate with one or more
15 neurological disorders. The invention also provides a method for treating a neurological disorder comprising the step of administering to a mammal in need of such treatment an amount of an antibody-like polypeptide of the invention that is sufficient to modulate ligand binding of a GPCR seven transmembrane receptor of the present invention in neurons of the mammal. In addition to administration of
20 antibody-like polypeptides, administration of natural ligands for GPCR polypeptides as well as modulators of GPCR polypeptide activity, such as small molecules that mimic, agonize or antagonize ligand-mediated GPCR polypeptide signaling, are contemplated. The expression pattern provides an indication that such molecules will have utility for treating neurological and/or psychiatric diseases, including but not
25 limited to schizophrenia, depression, anxiety, bipolar disease, affective disorders, attention deficit hyperactivity disorder/attention deficit disorder (ADHD/ADO), epilepsy, neuritis, neurasthenia, neuropathy, neuroses, Alzheimer's disease, Parkinson's disease, migraine, senile dementia, and the like. Treatment of individuals having any of these disorders is contemplated as an aspect of the invention.

30 Thus, in yet another embodiment, the invention provides genetic screening procedures that entail analyzing a person's genome -- in particular their

- 31 -

alleles for GPCR's of the invention -- to determine whether the individual possesses a genetic characteristic found in other individuals that are considered to be afflicted with, or at risk for, developing a mental disorder or disease of the brain that is suspected of having a hereditary component. For example, in one embodiment, the invention provides a method for determining a potential for developing a disorder affecting the brain in a human subject comprising the steps of analyzing the coding sequence of one or more GPCR genes from the human subject; and determining development potential for the disorder in said human subject from the analyzing step.

More particularly, the invention provides a method of screening a human subject to diagnose a disorder affecting the brain or genetic predisposition therefor, comprising the steps of: (a) assaying nucleic acid of a human subject to determine a presence or an absence of a mutation altering the amino acid sequence, expression, or biological activity of at least one seven transmembrane receptor that is expressed in the brain, wherein the seven transmembrane receptor comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 2, 4, 6, 8, 10, 12, 14, 16, 18, and 20, or an allelic variant thereof, and wherein the nucleic acid corresponds to the gene encoding the seven transmembrane receptor; and (b) diagnosing the disorder or predisposition from the presence or absence of said mutation, wherein the presence of a mutation altering the amino acid sequence, expression, or biological activity of allele in the nucleic acid correlates with an increased risk of developing the disorder. In preferred variations, the seven transmembrane receptor is CON202 comprising an amino acid sequence set forth in SEQ ID NO: 14, or an allelic variant thereof, and the disease is schizophrenia.

By "human subject" is meant any human being, human embryo, or human fetus. It will be apparent that methods of the present invention will be of particular interest to individuals that have themselves been diagnosed with a disorder affecting the brain or have relatives that have been diagnosed with a disorder affecting the brain.

By "screening for an increased risk" is meant determination of whether a genetic variation exists in the human subject that correlates with a greater likelihood of developing a disorder affecting the brain than exists for the human population as a

- 32 -

whole, or for a relevant racial or ethnic human sub-population to which the individual belongs. Both positive and negative determinations (i.e., determinations that a genetic predisposition marker is present or is absent) are intended to fall within the scope of screening methods of the invention. In preferred embodiments, the presence of a mutation altering the sequence or expression of at least one *CON202* seven transmembrane receptor allele in the nucleic acid is correlated with an increased risk of developing schizophrenia, whereas the absence of such a mutation is reported as a negative determination.

The "assaying" step of the invention may involve any techniques available for analyzing nucleic acid to determine its characteristics, including but not limited to well-known techniques such as single-strand conformation polymorphism analysis (SSCP) [Orita *et al.*, *Proc Natl. Acad. Sci. USA*, 86: 2766-2770 (1989)]; heteroduplex analysis [White *et al.*, *Genomics*, 12: 301-306 (1992)]; denaturing gradient gel electrophoresis analysis [Fischer *et al.*, *Proc. Natl. Acad. Sci. USA*, 80: 1579-1583 (1983); and Riesner *et al.*, *Electrophoresis*, 10: 377-389 (1989)]; DNA sequencing; RNase cleavage [Myers *et al.*, *Science*, 230: 1242-1246 (1985)]; chemical cleavage of mismatch techniques [Rowley *et al.*, *Genomics*, 30: 574-582 (1995); and Roberts *et al.*, *Nucl. Acids Res.*, 25: 3377-3378 (1997)]; restriction fragment length polymorphism analysis; single nucleotide primer extension analysis [Shumaker *et al.*, *Hum. Mutat.*, 7: 346-354 (1996); and Pastinen *et al.*, *Genome Res.*, 7: 606-614 (1997)]; 5' nuclease assays [Pease *et al.*, *Proc. Natl. Acad. Sci. USA*, 91:5022-5026 (1994)]; DNA Microchip analysis [Ramsay, G., *Nature Biotechnology*, 16: 40-48 (1999); and Chee *et al.*, U.S. Patent No. 5,837,832]; and ligase chain reaction [Whiteley *et al.*, U.S. Patent No. 5,521,065]. [See generally, Schafer and Hawkins, *Nature Biotechnology*, 16: 33-39 (1998).] All of the foregoing documents are hereby incorporated by reference in their entirety.

Thus, in one preferred embodiment involving screening *CON202* sequences, for example, the assaying step comprises at least one procedure selected from the group consisting of: (a) determining a nucleotide sequence of at least one codon of at least one *CON202* allele of the human subject; (b) performing a hybridization assay to determine whether nucleic acid from the human subject has a

- 33 -

nucleotide sequence identical to or different from one or more reference sequences;
(c) performing a polynucleotide migration assay to determine whether nucleic acid
from the human subject has a nucleotide sequence identical to or different from one or
more reference sequences; and (d) performing a restriction endonuclease digestion to
5 determine whether nucleic acid from the human subject has a nucleotide sequence
identical to or different from one or more reference sequences.

In a highly preferred embodiment, the assaying involves sequencing of
nucleic acid to determine nucleotide sequence thereof, using any available sequencing
technique. [See, e.g., Sanger *et al.*, *Proc. Natl. Acad. Sci. (USA)*, 74: 5463-5467
10 (1977) (dideoxy chain termination method); Mirzabekov, *TIBTECH*, 12: 27-32 (1994)
(sequencing by hybridization); Drmanac *et al.*, *Nature Biotechnology*, 16: 54-58
(1998); U.S. Patent No. 5,202,231; and *Science*, 260: 1649-1652 (1993) (sequencing
by hybridization); Kieleczawa *et al.*, *Science*, 258: 1787-1791 (1992) (sequencing by
primer walking); (Douglas *et al.*, *Biotechniques*, 14: 824-828 (1993) (Direct
15 sequencing of PCR products); and Akane *et al.*, *Biotechniques* 16: 238-241 (1994);
Maxam and Gilbert, *Meth. Enzymol.*, 65: 499-560 (1977) (chemical termination
sequencing), all incorporated herein by reference.] The analysis may entail sequencing
of the entire seven transmembrane receptor gene genomic DNA sequence, or portions
thereof; or sequencing of the entire seven transmembrane receptor coding sequence or
20 portions thereof. In some circumstances, the analysis may involve a determination of
whether an individual possesses a particular allelic variant, in which case sequencing
of only a small portion of nucleic acid -- enough to determine the sequence of a
particular codon characterizing the allelic variant -- is sufficient. This approach is
appropriate, for example, when assaying to determine whether one family member
25 inherited the same allelic variant that has been previously characterized for another
family member, or, more generally, whether a person's genome contains an allelic
variant that has been previously characterized and correlated with a mental disorder
having a heritable component.

In another highly preferred embodiment, the assaying step comprises
30 performing a hybridization assay to determine whether nucleic acid from the human
subject has a nucleotide sequence identical to or different from one or more reference

sequences. In a preferred embodiment, the hybridization involves a determination of whether nucleic acid derived from the human subject will hybridize with one or more oligonucleotides, wherein the oligonucleotides have nucleotide sequences that correspond identically to a portion of the GPCR gene sequence taught herein, such as the CON202 coding sequence set forth in SEQ ID NO: 14, or that correspond identically except for one mismatch. The hybridization conditions are selected to differentiate between perfect sequence complementarity and imperfect matches differing by one or more bases. Such hybridization experiments thereby can provide single nucleotide polymorphism sequence information about the nucleic acid from the human subject, by virtue of knowing the sequences of the oligonucleotides used in the experiments.

Several of the techniques outlined above involve an analysis wherein one performs a polynucleotide migration assay, *e.g.*, on a polyacrylamide electrophoresis gel (or in a capillary electrophoresis system), under denaturing or non-denaturing conditions. Nucleic acid derived from the human subject is subjected to gel electrophoresis, usually adjacent to (or co-loaded with) one or more reference nucleic acids, such as reference GPCR-encoding sequences having a coding sequence identical to all or a portion of SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, or 19 (or identical except for one known polymorphism). The nucleic acid from the human subject and the reference sequence(s) are subjected to similar chemical or enzymatic treatments and then electrophoresed under conditions whereby the polynucleotides will show a differential migration pattern, unless they contain identical sequences. [See generally Ausubel *et al.* (eds.), *Current Protocols in Molecular Biology*, New York: John Wiley & Sons, Inc. (1987-1999); and Sambrook *et al.*, (eds.), *Molecular Cloning, A Laboratory Manual*, Cold Spring Harbor, New York: Cold Spring Harbor Laboratory Press (1989), both incorporated herein by reference in their entirety.]

In the context of assaying, the term "nucleic acid of a human subject" is intended to include nucleic acid obtained directly from the human subject (*e.g.*, DNA or RNA obtained from a biological sample such as a blood, tissue, or other cell or fluid sample); and also nucleic acid derived from nucleic acid obtained directly from the human subject. By way of non-limiting examples, well known procedures

- 35 -

exist for creating cDNA that is complementary to RNA derived from a biological sample from a human subject, and for amplifying (*e.g.*, via polymerase chain reaction (PCR)) DNA or RNA derived from a biological sample obtained from a human subject. Any such derived polynucleotide which retains relevant nucleotide sequence information of the human subject's own DNA/RNA is intended to fall within the definition of "nucleic acid of a human subject" for the purposes of the present invention.

In the context of assaying, the term "mutation" includes addition, deletion, and/or substitution of one or more nucleotides in the GPCR gene sequence (*e.g.*, as compared to the seven transmembrane receptor-encoding sequences set forth in SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, or 19) and other polymorphisms that occur in introns (where introns exist) and that are identifiable via sequencing, restriction fragment length polymorphism, or other techniques. The various activity examples provided herein permit determination of whether a mutation modulates activity of the relevant receptor in the presence or absence of various test substances.

In a related embodiment, the invention provides methods of screening a person's genotype with respect to GPCR's of the invention, and correlating such genotypes with diagnoses for disease or with predisposition for disease (for genetic counseling). For example, the invention provides a method of screening for a CON202 hereditary schizophrenia genotype in a human patient, comprising the steps of: (a) providing a biological sample comprising nucleic acid from the patient, the nucleic acid including sequences corresponding to said patient's CON202 alleles; (b) analyzing the nucleic acid for the presence of a mutation or mutations; (c) determining a CON202 genotype from the analyzing step; and (d) correlating the presence of a mutation in a CON202 allele with a hereditary schizophrenia genotype. In a preferred embodiment, the biological sample is a cell sample containing human cells that contain genomic DNA of the human subject. The analyzing can be performed analogously to the assaying described in preceding paragraphs. For example, the analyzing comprises sequencing a portion of the nucleic acid (*e.g.*, DNA or RNA), the portion comprising at least one codon of the CON202 alleles.

- 36 -

Although more time consuming and expensive than methods involving nucleic acid analysis, the invention also may be practiced by assaying protein of a human subject to determine the presence or absence of an amino acid sequence variation in GPCR protein from the human subject. Such protein analyses may be performed, e.g., by fragmenting GPCR protein via chemical or enzymatic methods and sequencing the resultant peptides; or by Western analyses using an antibody having specificity for a particular allelic variant of the GPCR.

The invention also provides materials that are useful for performing methods of the invention. For example, the present invention provides oligonucleotides useful as probes in the many analyzing techniques described above. In general, such oligonucleotide probes comprise 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, or 50 nucleotides that have a sequence that is identical, or exactly complementary, to a portion of a human GPCR gene sequence taught herein (or allelic variant thereof), or that is identical or exactly complementary except for one nucleotide substitution. In a preferred embodiment, the oligonucleotides have a sequence that corresponds in the foregoing manner to a human GPCR coding sequence taught herein, and in particular, the coding sequences set forth in SEQ ID NOs: 1, 3, 5, 7, 9, 11, 13, 15, 17, or 19. In one variation, an oligonucleotide probe of the invention is purified and isolated. In another variation, the oligonucleotide probe is labeled, e.g., with a radioisotope, chromophore, or fluorophore. In yet another variation, the probe is covalently attached to a solid support. [See generally Ausubel *et al.* And Sambrook *et al.*, *supra*.]

In a related embodiment, the invention provides kits comprising reagents that are useful for practicing methods of the invention. For example, the invention provides a kit for screening a human subject to diagnose schizophrenia or a genetic predisposition therefor, comprising, in association: (a) an oligonucleotide useful as a probe for identifying polymorphisms in a human CON202 seven transmembrane receptor gene, the oligonucleotide comprising 6-50 nucleotides that have a sequence that is identical or exactly complementary to a portion of a human CON202 gene sequence or CON202 coding sequence, except for one sequence

- 37 -

difference selected from the group consisting of a nucleotide addition, a nucleotide deletion, or nucleotide substitution; and (b) a media packaged with the oligonucleotide containing information identifying polymorphisms identifiable with the probe that correlate with schizophrenia or a genetic predisposition therefor.

5 Exemplary information-containing media include printed paper package inserts or packaging labels; and magnetic and optical storage media that are readable by computers or machines used by practitioners who perform genetic screening and counseling services. The practitioner uses the information provided in the media to correlate the results of the analysis with the oligonucleotide with a diagnosis. In a
10 preferred variation, the oligonucleotide is labeled.

In still another embodiment, the invention provides methods of identifying those allelic variants of GPCR's of the invention that correlate with mental disorders. For example, the invention provides a method of identifying a seven transmembrane allelic variant that correlates with a mental disorder, comprising steps
15 of: (a) providing a biological sample comprising nucleic acid from a human patient diagnosed with a mental disorder, or from the patient's genetic progenitors or progeny; (b) analyzing the nucleic acid for the presence of a mutation or mutations in at least one seven transmembrane receptor that is expressed in the brain, wherein the at least one seven transmembrane receptor comprises an amino acid sequence selected
20 from the group consisting of SEQ ID NOs: 2, 4, 6, 8, 10, 12, 14, 16, 18, and 20, or an allelic variant thereof, and wherein the nucleic acid includes sequence corresponding to the gene or genes encoding the at least one seven transmembrane receptor; (c) determining a genotype for the patient for the at least one seven transmembrane receptor from said analyzing step; and (d) identifying an allelic variant that correlates
25 with the mental disorder from the determining step. To expedite this process, it may be desirable to perform linkage studies in the patients (and possibly their families) to correlate chromosomal markers with disease states. The chromosomal localization data provided herein facilitates identifying an involved GPCR with a chromosomal marker.

30 The foregoing method can be performed to correlate GPCR's of the invention to a number of disorders having hereditary components that are causative or

- 38 -

that predispose persons to the disorder. For example, in one preferred variation, the disorder is schizophrenia, and the at least one seven transmembrane receptor comprises CON202 having an amino acid sequence set forth in SEQ ID NO: 14, or an allelic variant thereof.

5 Also contemplated as part of the invention are polynucleotides that comprise the allelic variant sequences identified by such methods, and polypeptides encoded by the allelic variant sequences, and oligonucleotide and oligopeptide fragments thereof that embody the mutations that have been identified. Such materials are useful in *in vitro* cell-free and cell-based assays for identifying lead compounds
10 and therapeutics for treatment of the disorders. For example, the variants are used in activity assays, binding assays, and assays to screen for activity modulators described herein. In one preferred embodiment, the invention provides a purified and isolated polynucleotide comprising a nucleotide sequence encoding a CON202 receptor allelic variant identified according to the methods described above; and an oligonucleotide
15 that comprises the sequences that differentiate the allelic variant from the CON202 sequences set forth in SEQ ID NOs: 13 and 14. The invention also provides a vector comprising the polynucleotide (preferably an expression vector); and a host cell transformed or transfected with the polynucleotide or vector. The invention also provides an isolated cell line that is expressing the allelic variant GPCR polypeptide;
20 purified cell membranes from such cells; purified polypeptide; and synthetic peptides that embody the allelic variation amino acid sequence. In one particular embodiment, the invention provides a purified polynucleotide comprising a nucleotide sequence encoding a CON202 seven transmembrane receptor protein of a human that is affected with schizophrenia; wherein said polynucleotide hybridizes to the complement of
25 SEQ ID NO: 13 under the following hybridization conditions: (a) hybridization for 16 hours at 42°C in a hybridization solution comprising 50% formamide, 1% SDS, 1 M NaCl, 10% dextran sulfate and (b) washing 2 times for 30 minutes at 60°C in a wash solution comprising 0.1x SSC and 1% SDS; and wherein the polynucleotide encodes a CON202 amino acid sequence that differs from SEQ ID NO: 14 at at least one
30 residue.

An exemplary assay for using the allelic variants is a method for identifying a modulator of CON202 biological activity, comprising the steps of: (a) contacting a cell expressing the allelic variant in the presence and in the absence of a putative modulator compound; (b) measuring CON202 biological activity in the cell; and (c) identifying a putative modulator compound in view of decreased or increased CON202 biological activity in the presence versus absence of the putative modulator.

In still another example, the invention provides for a method of diagnosing schizophrenia or a susceptibility to schizophrenia comprising the steps of: determining the presence or amount of expression of CON202 polypeptide as set out as SEQ ID NO: 14 or the polypeptide encoded by the nucleic acid molecule having SEQ ID NO: 13 in a sample; and comparing the level of CON202 polypeptide in a biological, tissue or cellular sample from normal subjects or the subject at an earlier time, wherein the susceptibility to schizophrenia is based on the presence or amount of CON202 polypeptide expression.

The invention also provides for a method of treating schizophrenia comprising the step of administering to a human diagnosed with schizophrenia an amount of a modulator of CON202 receptor activity sufficient to modulate CON202 receptor activity or CON202 ligand binding in said human.

The invention also provides assays to identify compounds that bind GPCR seven transmembrane receptors. One such assay comprises the steps of: (a) contacting a composition comprising one of the GPCR seven transmembrane receptor polypeptides of the invention with a compound suspected of binding a GPCR polypeptide of the invention; and (b) measuring binding between the compound and the GPCR polypeptide. In one variation, the composition comprises a cell expressing a GPCR polypeptide of the invention on its surface. In another variation, an isolated GPCR polypeptide of the invention or cell membranes comprising a GPCR polypeptide of the invention are employed. The binding may be measured directly, e.g., using a labeled compound, or may be measured indirectly by several techniques, including measuring intracellular signaling of a GPCR polypeptide of the invention induced by the compound (or measuring changes in the level of GPCR polypeptide signaling).

The invention also provides a method for identifying a modulator of binding between a GPCR seven transmembrane receptor of the invention and a GPCR polypeptide binding partner, comprising the steps of: (a) contacting a GPCR polypeptide binding partner and a composition comprising one of the GPCR seven transmembrane receptors of the invention in the presence and in the absence of a putative modulator compound; (b) detecting binding between the binding partner and the GPCR polypeptide of the invention; and (c) identifying a putative modulator compound in view of decreased or increased binding between the binding partner and the GPCR polypeptide in the presence of the putative modulator, as compared to binding in the absence of the putative modulator.

GPCR polypeptide binding partners that stimulate GPCR seven transmembrane receptors of the present invention are useful as agonists in disease states characterized by insufficient GPCR polypeptide signaling (*e.g.*, as a result of insufficient expression of active GPCR polypeptide ligand). GPCR polypeptide binding partners that block ligand-mediated GPCR polypeptide signaling are useful as GPCR polypeptide antagonists to treat disease states characterized by excessive GPCR polypeptide signaling.

Additional features and variations of the invention will be apparent to those skilled in the art from the entirety of this application, including the detailed description, and all such features are intended as aspects of the invention. Likewise, features of the invention described herein can be re-combined into additional embodiments that also are intended as aspects of the invention, irrespective of whether the combination of features is specifically mentioned above as an aspect or embodiment of the invention. Also, only such limitations which are described herein as critical to the invention should be viewed as such; variations of the invention lacking limitations which have not been described herein as critical are intended as aspects of the invention.

In addition to the foregoing, the invention includes, as an additional aspect, all embodiments of the invention narrower in scope in any way than the variations specifically mentioned above. Although the applicant(s) invented the full scope of the claims appended hereto, the claims appended hereto are not intended to

- 41 -

encompass within their scope the prior art work of others. Therefore, in the event that statutory prior art within the scope of a claim is brought to the attention of the applicants by a Patent Office or other entity or individual, the applicant(s) reserve the right to exercise amendment rights under applicable patent laws to redefine the subject matter of such a claim to specifically exclude such statutory prior art or obvious variations of statutory prior art from the scope of such a claim. Variations of the invention defined by such amended claims also are intended as aspects of the invention.

DETAILED DESCRIPTION OF THE INVENTION

The present invention provides purified and isolated polynucleotides (e.g., DNA sequences and RNA transcripts, both sense and complementary antisense strands, both single and double stranded, including splice variants thereof) encoding human G protein-coupled receptors referred to herein as GPCR polypeptides. DNA polynucleotides of the invention include genomic DNA, cDNA, and DNA that has been chemically synthesized in whole or in part. "Synthesized" as used herein and understood in the art, refers to polynucleotides produced by purely chemical, as opposed to enzymatic, methods. "Wholly" synthesized DNA sequences are therefore produced entirely by chemical means, and "partially" synthesized DNAs embrace those wherein only portions of the resulting DNA were produced by chemical means.

Genomic DNA of the invention comprises the protein coding region for a polypeptide of the invention and is also intended to include allelic variants thereof. It is widely understood that, for many genes, genomic DNA is transcribed into RNA transcripts that undergo one or more splicing events wherein intron (*i.e.*, non-coding regions) of the transcripts are removed, or "spliced out." RNA transcripts that can be spliced by alternative mechanisms, and therefore be subject to removal of different RNA sequences but still encode a GPCR polypeptide of the present invention, are referred to in the art as splice variants which are embraced by the invention. Splice variants comprehended by the invention therefore are encoded by the same original genomic DNA sequences but arise from distinct mRNA transcripts. Allelic variants are modified forms of a wild type gene sequence, the modification

resulting from recombination during chromosomal segregation or exposure to conditions which give rise to genetic mutation. Allelic variants, like wild type genes, are naturally occurring sequences (as opposed to non-naturally occurring variants which arise from *in vitro* manipulation).

5 The invention also comprehends cDNA that is obtained through reverse transcription of an RNA polynucleotide encoding a GPCR of the present invention (conventionally followed by second strand synthesis of a complementary strand to provide a double-stranded DNA).

10 A preferred DNA sequence encoding a human GPCR polypeptide is set out in SEQ ID NO: 1, wherein nucleotides 157 to 1122 represent the CON193 coding sequence, with termination codon (surrounded by upstream and downstream untranslated sequences). Another preferred DNA sequence encoding a human GPCR polypeptide is set out in SEQ ID NO: 3, wherein nucleotides 1 to 1014 represent the CON166 coding sequence and stop codon. Still another preferred DNA sequence
15 encoding a human GPCR polypeptide is set out in SEQ ID NO: 5, wherein nucleotides 691 to 1845 represent the CON103 coding sequence with stop codon (surrounded by upstream and downstream untranslated sequences). Another preferred DNA sequence encoding a human GPCR polypeptide is set out in SEQ ID NO: 7, wherein nucleotides 146 to 1147 represent the CON203 coding sequence with
20 stop codon (surrounded by upstream and downstream untranslated sequences). A preferred DNA sequence encoding a human GPCR polypeptide is set out in SEQ ID NO: 9, wherein nucleotides 1 to 957 represent the CON198 coding sequence with stop codon. Another preferred DNA sequence encoding a human GPCR polypeptide is set out in SEQ ID NO: 11, wherein nucleotides 1 to 924 represent the CON197 coding
25 sequence with stop codon (followed by downstream untranslated sequences). A preferred DNA sequence encoding a human GPCR polypeptide is set out in SEQ ID NO: 13, wherein nucleotides 266 to 1378 represent the CON202 coding sequence and termination codon (surrounded by upstream and downstream untranslated sequences). A preferred DNA sequence encoding a human GPCR polypeptide is set out in SEQ ID
30 NO: 15, wherein nucleotides 1 to 1191 represent the CON222 coding sequence and termination codon. A preferred DNA sequence encoding a human GPCR polypeptide

- 43 -

is set out in SEQ ID NO: 17, wherein nucleotides 13 to 1089 represent the CON215 coding sequence and termination codon (surrounded by upstream and downstream untranslated sequences). A preferred DNA sequence encoding a human GPCR polypeptide is set out in SEQ ID NO: 19, wherein nucleotides 42 to 1157 represent
5 the CON217 coding sequence (surrounded by upstream and downstream untranslated sequences). The foregoing sequences without their termination codons also comprise preferred sequences.

The worker of skill in the art will readily appreciate that the preferred DNA of the invention comprises a double stranded molecule, for example the
10 molecule having any one of the sequences set forth in SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, or 19 (or coding portions thereof) along with the complementary molecule (the "non-coding strand" or "complement") having a sequence deducible from the sequence of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, or 19 according to Watson-Crick base pairing rules for DNA. Also preferred are other polynucleotides encoding
15 the GPCR polypeptides of the invention set forth in SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18 and 20 which differ in sequence from the polynucleotide of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, or 19, respectively, by virtue of the well-known degeneracy of the universal genetic code.

The invention further embraces species, preferably mammalian,
20 homologs of the human GPCR DNAs. Species homologs, sometimes referred to as "orthologs," in general, share at least 35%, at least 40%, at least 45%, at least 50%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 98%, or at least 99% homology with human DNA of the invention. Percent sequence "homology" with respect to polynucleotides of the
25 invention is defined herein as the percentage of nucleotide bases in the candidate sequence that are identical to nucleotides in the GPCR sequence set forth in any one of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, or 19 after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity.

The polynucleotide sequence information provided by the invention
30 makes possible large scale expression of the encoded polypeptide by techniques well known and routinely practiced in the art. Polynucleotides of the invention also permit

identification and isolation of polynucleotides encoding related GPCR polypeptides, such as human allelic variants and species homologs, by well known techniques including Southern and/or Northern hybridization, and polymerase chain reaction (PCR). Examples of related polynucleotides include human and non-human genomic sequences, including allelic variants, as well as polynucleotides encoding polypeptides homologous to GPCR polypeptides and structurally related the polypeptides sharing one or more biological, immunological, and/or physical properties of the GPCR polypeptides. Non-human species genes encoding proteins homologous to GPCR polypeptides can also be identified by Southern and/or PCR analysis and are useful in animal models for GPCR-related disorders. Knowledge of the sequence of a human GPCR DNA also makes possible, through use of Southern hybridization or polymerase chain reaction (PCR), the identification of genomic DNA sequences encoding GPCR expression control regulatory sequences such as promoters, operators, enhancers, repressors, and the like. Polynucleotides of the invention are also useful in hybridization assays to detect the capacity of cells to express GPCR polypeptides. Polynucleotides of the invention may also be the basis for diagnostic methods useful for identifying a genetic alteration(s) in a GPCR locus that underlies a disease state or states, which information is useful both for diagnosis and for selection of therapeutic strategies.

The disclosure herein of full length polynucleotides encoding GPCR polypeptides of the present invention makes readily available to the worker of ordinary skill in the art every possible fragment of the full length polynucleotides. The invention therefore provides fragments of GPCR-encoding polynucleotides comprising at least 14-15, and preferably at least 18, 20, 25, 50, or 75 consecutive nucleotides of a polynucleotide encoding GPCR polypeptides. Preferably, fragment polynucleotides of the invention comprise sequences unique to the GPCR-encoding polynucleotide sequence, and therefore hybridize under highly stringent or moderately stringent conditions only (*i.e.*, "specifically") to polynucleotides encoding GPCR polypeptides (or fragments thereof). Polynucleotide fragments of genomic sequences of the invention comprise not only sequences unique to the coding region, but also include fragments of the full length sequence derived from introns, regulatory regions,

and/or other non-translated sequences. Sequences unique to polynucleotides of the invention are recognizable through sequence comparison to other known polynucleotides, and can be identified through use of alignment programs routinely utilized in the art, *e.g.*, those made available in public sequence databases. Such sequences also are recognizable from Southern and Northern hybridization analyses to determine the number of fragments of genomic DNA and RNA to which a polynucleotide will hybridize. Polynucleotides of the invention can be labeled in a manner that permits their detection, including radioactive, fluorescent, and enzymatic labeling.

Fragment polynucleotides are particularly useful as probes for detection of full length or other fragment GPCR polynucleotides. One or more fragment polynucleotides can be included in kits that are used to detect the presence of a polynucleotide encoding a GPCR polypeptide, or used to detect variations in a polynucleotide sequences encoding GPCR polypeptides.

The invention also embraces DNAs encoding GPCR polypeptides which DNAs hybridize under moderately stringent or high stringency conditions to the non-coding strand, or complement, of the polynucleotide in any one of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17 or 19.

Exemplary highly stringent hybridization conditions are as follows: hybridization at 42°C in a hybridization solution comprising 50% formamide, 1% SDS, 1 M NaCl, 10% Dextran sulfate, and washing twice for 30 minutes at 60°C in a wash solution comprising 0.1x SSC and 1% SDS. It is understood in the art that conditions of equivalent stringency can be achieved through variation of temperature and buffer, or salt concentration as described Ausubel, *et al.* (Eds.), *Protocols in Molecular Biology*, John Wiley & Sons (1994), pp. 6.0.3 to 6.4.10. Modifications in hybridization conditions can be empirically determined or precisely calculated based on the length and the percentage of guanosine/cytosine (GC) base pairing of the probe. The hybridization conditions can be calculated as described in Sambrook *et al.*, (Eds.), *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory Press: Cold Spring Harbor, New York (1989), pp. 9.47 to 9.51.

Autonomously replicating recombinant expression constructs such as plasmid and viral DNA vectors incorporating polynucleotides of the invention are also provided. Expression constructs wherein GPCR-encoding polynucleotides are operatively linked to an endogenous or exogenous expression control DNA sequence and a transcription terminator are also provided. Expression control DNA sequences include promoters, enhancers, and operators, and are generally selected based on the expression systems in which the expression construct is to be utilized. Preferred promoter and enhancer sequences are generally selected for the ability to increase gene expression, while operator sequences are generally selected for the ability to regulate gene expression. Expression constructs of the invention may also include sequences encoding one or more selectable markers that permit identification of host cells bearing the construct. Expression constructs may also include sequences that facilitate, and preferably promote, homologous recombination in a host cell. Preferred constructs of the invention also include sequences necessary for replication in a host cell.

Expression constructs are preferably utilized for production of an encoded protein, but also may be utilized simply to amplify GPCR-encoding polynucleotide sequences.

According to another aspect of the invention, host cells are provided, including prokaryotic and eukaryotic cells, comprising a polynucleotide of the invention (or vector of the invention) in a manner which permits expression of the encoded GPCR polypeptide. Polynucleotides of the invention may be introduced into the host cell as part of a circular plasmid, or as linear DNA comprising an isolated protein coding region or a viral vector. Methods for introducing DNA into the host cell well known and routinely practiced in the art include transformation, transfection, electroporation, nuclear injection, or fusion with carriers such as liposomes, micelles, ghost cells, and protoplasts. Expression systems of the invention include bacterial, yeast, fungal, plant, insect, invertebrate, and mammalian cells systems.

Host cells of the invention are a valuable source of immunogen for development of antibodies specifically immunoreactive with GPCR polypeptides. Host cells of the invention are also useful in methods for large scale production of

GPCR polypeptides wherein the cells are grown in a suitable culture medium and the desired polypeptide products are isolated from the cells or from the medium in which the cells are grown by purification methods known in the art, *e.g.*, conventional chromatographic methods including immunoaffinity chromatography, receptor
5 affinity chromatography, hydrophobic interaction chromatography, lectin affinity chromatography, size exclusion filtration, cation or anion exchange chromatography, high pressure liquid chromatography (HPLC), reverse phase HPLC, and the like. Still other methods of purification include those wherein the desired protein is expressed and purified as a fusion protein having a specific tag, label, or chelating moiety that is
10 recognized by a specific binding partner or agent. The purified protein can be cleaved to yield the desired protein, or be left as an intact fusion protein. Cleavage of the fusion component may produce a form of the desired protein having additional amino acid residues as a result of the cleavage process.

Knowledge of GPCR DNA sequences allows for modification of cells
15 to permit, or increase, expression of endogenous GPCR. Cells can be modified (*e.g.*, by homologous recombination) to provide increased expression by replacing, in whole or in part, the naturally occurring GPCR promoter with all or part of a heterologous promoter so that the cells express GPCR polypeptides at higher levels. The heterologous promoter is inserted in such a manner that it is operatively linked to
20 endogenous GPCR polypeptide encoding sequences. [See, for example, PCT International Publication No. WO 94/12650, PCT International Publication No. WO 92/20808, and PCT International Publication No. WO 91/09955.] It is also contemplated that, in addition to heterologous promoter DNA, amplifiable marker DNA (*e.g.*, *ada*, *dhfr*, and the multifunctional CAD gene which encodes carbamyl
25 phosphate synthase, aspartate transcarbamylase, and dihydroorotase) and/or intron DNA may be inserted along with the heterologous promoter DNA. If linked to the GPCR coding sequence, amplification of the marker DNA by standard selection methods results in co-amplification of the GPCR coding sequences in the cells.

The DNA sequence information provided by the present invention also
30 makes possible the development through, *e.g.* homologous recombination or "knock-out" strategies [Capecchi, *Science* 244: 1288-1292 (1989)], of animals that

fail to express functional GPCR polypeptides or that express a variant of GPCR polypeptides. Such animals (especially small laboratory animals such as rats, rabbits, and mice) are useful as models for studying the *in vivo* activities of GPCR polypeptides and modulators of GPCR polypeptides.

5 Also made available by the invention are anti-sense polynucleotides which recognize and hybridize to polynucleotides encoding GPCR polypeptides. Full length and fragment anti-sense polynucleotides are provided. Fragment anti-sense molecules of the invention include those which specifically recognize and hybridize to GPCR RNA (as determined by sequence comparison of DNA encoding GPCR
10 polypeptides to DNA encoding other known molecules). Identification of sequences unique to GPCR-encoding polynucleotides, can be deduced through use of any publicly available sequence database, and/or through use of commercially available sequence comparison programs. The uniqueness of selected sequences in an entire genome can be further verified by hybridization analyses. After identification of the
15 desired sequences, isolation through restriction digestion or amplification using any of the various polymerase chain reaction techniques well known in the art can be performed. Antisense polynucleotides are particularly relevant to regulating expression of GPCR polypeptides by those cells expressing GPCR mRNA.

 Antisense nucleic acids (preferably 10 to 20 base pair oligonucleotides)
20 capable of specifically binding to GPCR expression control sequences or GPCR RNA are introduced into cells (*e.g.*, by a viral vector or colloidal dispersion system such as a liposome). The antisense nucleic acid binds to the GPCR target nucleotide sequence in the cell and prevents transcription or translation of the target sequence. Phosphorothioate and methylphosphonate antisense oligonucleotides are specifically
25 contemplated for therapeutic use by the invention. The antisense oligonucleotides may be further modified by poly-L-lysine, transferrin polylysine, or cholesterol moieties at their 5' end. Suppression of GPCR polypeptide expression at either the transcriptional or translational level is useful to general cellular and/or animal models for diseases characterized by aberrant expression. Suppression of GPCR polypeptide
30 expression at either the transcriptional or translational level is useful to generate

- 49 -

cellular animal models for diseases characterized by aberrant GPCR polypeptide expression.

The GPCR polynucleotide and polypeptide sequences taught in the present invention facilitate the design of novel transcription factors for modulating GPCR polypeptide expression in native cells and animals, and cells transformed or transfected with GPCR polynucleotides. For example, the Cys₂-His₂ zinc finger proteins, which bind DNA via their zinc finger domains, have been shown to be amenable to structural changes that lead to the recognition of different target sequences. These artificial zinc finger proteins recognize specific target sites with high affinity and low dissociation constants, and are able to act as gene switches to modulate gene expression. Knowledge of the particular GPCR target sequence of the present invention facilitates the engineering of zinc finger proteins specific for the target sequence using known methods such as a combination of structure-based modeling and screening of phage display libraries [Segal *et al.*, *Proc Natl Acad Sci USA* 96: 2758-2763 (1999); Liu *et al.*, *Proc Natl Acad Sci USA* 94: 5525-30 (1997); Greisman and Pabo *Science* 275: 657-61 (1997); Choo *et al.*, *J Mol Biol* 273: 525-32 (1997)]. Each zinc finger domain usually recognizes three or more base pairs. Since a recognition sequence of 18 base pairs is generally sufficient in length to render it unique in any known genome, a zinc finger protein consisting of 6 tandem repeats of zinc fingers would be expected to ensure specificity for a particular sequence [Segal *et al.*, *Proc Natl Acad Sci USA* 96: 2758-2763 (1999)]. The artificial zinc finger repeats, designed based on GPCR polynucleotide sequences, are fused to activation or repression domains to promote or suppress GPCR polypeptides expression [Liu *et al.*, *Proc Natl Acad Sci USA* 94: 5525-30 (1997)]. Alternatively, the zinc finger domains can be fused to the TATA box-binding factor (TBP) with varying lengths of linker region between the zinc finger peptide and the TBP to create either transcriptional activators or repressors [Kim *et al.*, *Proc Natl Acad Sci USA* 94: 3616-3620 (1997)]. Such proteins, and polynucleotides that encode them, have utility for modulating GPCR polypeptide expression *in vivo* in both native cells, animals and humans; and/or cells transfected with GPCR polynucleotide-encoding sequences. The novel transcription factor can be delivered to the target cells by transfecting constructs that

express the transcription factor (gene therapy), or by introducing the protein.

Engineered zinc finger proteins can also be designed to bind RNA sequences for use in therapeutics as alternatives to antisense or catalytic RNA methods [McColl *et al.*, *Proc Natl Acad Sci USA* 96:9521-6 (1999); Wu *et al.*, *Proc Natl Acad Sci USA* 92:344-348 (1995)]. The present invention contemplates methods of designing such transcription factors based on the gene sequence of the invention, as well as customized zinc finger proteins, that are useful to modulate GPCR polypeptide expression in cells (native or transformed) whose genetic complement includes these sequences.

The invention also provides purified and isolated mammalian GPCR polypeptides encoded by a polynucleotide of the invention. Presently preferred is a human GPCR polypeptide comprising the amino acid sequence set out in any one of SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18 or 20.

The invention also embraces polypeptides that have at least 99%, at least 95%, at least 90%, at least 85%, at least 80%, at least 75%, at least 70%, at least 65%, at least 60%, at least 55% or at least 50% identity and/or homology to a preferred polypeptide of the invention. Percent amino acid sequence "identity" with respect to the preferred polypeptide of the invention is defined herein as the percentage of amino acid residues in the candidate sequence that are identical with the residues in a GPCR polypeptide sequence after aligning both sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity, and not considering any conservative substitutions as part of the sequence identity. Percent sequence "homology" with respect to the preferred polypeptide of the invention is defined herein as the percentage of amino acid residues in the candidate sequence that are identical with the residues in a GPCR sequence after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity, and also considering any conservative substitutions as part of the sequence identity.

In one aspect, percent homology is calculated as the percentage of amino acid residues in the smaller of two sequences which align with identical amino acid residue in the sequence being compared, when four gaps in a length of 100 amino

acids may be introduced to maximize alignment [Dayhoff, in *Atlas of Protein Sequence and Structure*, Vol. 5, p. 124, National Biochemical Research Foundation, Washington, D.C. (1972), incorporated herein by reference].

Polypeptides of the invention may be isolated from natural cell
5 sources or may be chemically synthesized, but are preferably produced by recombinant procedures involving host cells of the invention. Use of mammalian host cells is expected to provide for such post-translational modifications (*e.g.*, glycosylation, truncation, lipidation, and phosphorylation) as may be needed to confer optimal biological activity on recombinant expression products of the invention.
10 Glycosylated and non-glycosylated forms of GPCR polypeptides are embraced.

The invention also embraces variant (or analog) GPCR polypeptides. In one example, insertion variants are provided wherein one or more amino acid residues supplement a GPCR amino acid sequence. Insertions may be located at either or both termini of the protein, or may be positioned within internal regions of
15 the GPCR amino acid sequence. Insertional variants with additional residues at either or both termini can include for example, fusion proteins and proteins including amino acid tags or labels.

Insertion variants include GPCR polypeptides wherein one or more amino acid residues are added to a GPCR amino acid sequence, or to a biologically
20 active fragment thereof.

Variant products of the invention also include mature GPCR polypeptide products, *i.e.*, GPCR polypeptide products wherein leader or signal sequences are removed, with additional amino terminal residues. The additional amino terminal residues may be derived from another protein, or may include one or
25 more residues that are not identifiable as being derived from a specific proteins. GPCR polypeptide products with an additional methionine residue at position -1 (Met⁻¹-GPCR) are contemplated, as are variants with additional methionine and lysine residues at positions -2 and -1 (Met⁻²-Lys⁻¹-GPCR). Variants of GPCR polypeptide with additional Met, Met-Lys, Lys residues (or one or more basic residues in general)
30 are particularly useful for enhanced recombinant protein production in bacterial host cell.

The invention also embraces GPCR polypeptide variants having additional amino acid residues which result from use of specific expression systems. For example, use of commercially available vectors that express a desired polypeptide as part of glutathione-S-transferase (GST) fusion product provides the desired polypeptide having an additional glycine residue at position -1 after cleavage of the GST component from the desired polypeptide. Variants which result from expression in other vector systems are also contemplated.

Insertional variants also include fusion proteins wherein the amino and/or carboxy termini of a GPCR polypeptide is fused to another polypeptide.

In another aspect, the invention provides deletion variants wherein one or more amino acid residues in a GPCR polypeptide are removed. Deletions can be effected at one or both termini of the GPCR polypeptide, or with removal of one or more residues within the GPCR amino acid sequence. Deletion variants, therefore, include all fragments of a GPCR polypeptide.

The invention also embraces polypeptide fragments of the sequence set out in SEQ ID NO: 2 wherein the fragments maintain biological (e.g., ligand binding and/or intracellular signaling) or immunological properties of a GPCR polypeptide. Fragments comprising at least 5, 10, 15, 20, 25, 30, 35, or 40 consecutive amino acids of SEQ ID NO: 2 are comprehended by the invention. Preferred polypeptide fragments display antigenic properties unique to or specific for human GPCR and its allelic and species homologs. Fragments of the invention having the desired biological and immunological properties can be prepared by any of the methods well known and routinely practiced in the art.

In still another aspect, the invention provides substitution variants of GPCR polypeptides. Substitution variants include those polypeptides wherein one or more amino acid residues of a GPCR polypeptide are removed and replaced with alternative residues. In one aspect, the substitutions are conservative in nature, however, the invention embraces substitutions that are also non-conservative. Conservative substitutions for this purpose may be defined as set out in Tables A, B, or C below.

- 53 -

Variant polypeptides include those wherein conservative substitutions have been introduced by modification of polynucleotides encoding polypeptides of the invention. Amino acids can be classified according to physical properties and contribution to secondary and tertiary protein structure. A conservative substitution is recognized in the art as a substitution of one amino acid for another amino acid that has similar properties. Exemplary conservative substitutions are set out in Table A (from WO 97/09433, page 10, published March 13, 1997 (PCT/GB96/02197, filed 9/6/96), immediately below.

10

Table A

Conservative Substitutions I

SIDE CHAIN	
<u>CHARACTERISTIC</u>	<u>AMINO ACID</u>
Aliphatic	
Non-polar	G A P I L V
Polar - uncharged	C S T M N Q
Polar - charged	D E K R
Aromatic	H F W Y
Other	N Q D E

20

Alternatively, conservative amino acids can be grouped as described in Lehninger, [Biochemistry, Second Edition; Worth Publishers, Inc. NY:NY (1975), pp.71-77] as set out in Table B, immediately below.

25

Table B
Conservative Substitutions II

5	SIDE CHAIN	
	<u>CHARACTERISTIC</u>	<u>AMINO ACID</u>
	Non-polar (hydrophobic)	
	A. Aliphatic:	A L I V P
10	B. Aromatic:	F W
	C. Sulfur-containing:	M
	D. Borderline:	G
	Uncharged-polar	
	A. Hydroxyl:	S T Y
15	B. Amides:	N Q
	C. Sulfhydryl:	C
	D. Borderline:	G
	Positively Charged (Basic):	K R H
20	Negatively Charged (Acidic):	D E

As still an another alternative, exemplary conservative substitutions are set out in Table C, immediately below.

Table C
Conservative Substitutions III

	<u>Original</u> <u>Residue</u>	<u>Exemplary Substitution</u>
5	Ala (A)	Val, Leu, Ile
	Arg (R)	Lys, Gln, Asn
	Asn (N)	Gln, His, Lys, Arg
	Asp (D)	Glu
10	Cys (C)	Ser
	Gln (Q)	Asn
	Glu (E)	Asp
	His (H)	Asn, Gln, Lys, Arg
	Ile (I)	Leu, Val, Met, Ala, Phe,
15	Leu (L)	Ile, Val, Met, Ala, Phe
	Lys (K)	Arg, Gln, Asn
	Met (M)	Leu, Phe, Ile
	Phe (F)	Leu, Val, Ile, Ala
	Pro (P)	Gly
20	Ser (S)	Thr
	Thr (T)	Ser
	Trp (W)	Tyr
	Tyr (Y)	Trp, Phe, Thr, Ser
	Val (V)	Ile, Leu, Met, Phe, Ala

25

GPCR polypeptide variants that display ligand binding properties of native GPCR polypeptides and are expressed at higher levels, and variants that provide for constitutive active receptor are particularly useful in assays of the

invention. Such variants also are useful in cellular and animal models for diseases characterized by aberrant GPCR polypeptide expression/activity.

It should be understood that the definition of polypeptides of the invention is intended to include polypeptides bearing modifications other than insertion, deletion, or substitution of amino acid residues. By way of example, the modifications may be covalent in nature, and include for example, chemical bonding with polymers, lipids, other organic, and inorganic moieties. Such derivatives may be prepared to increase circulating half-life of a polypeptide, or may be designed to improve targeting capacity for the polypeptide to desired cells, tissues, or organs.

Similarly, the invention further embraces GPCR polypeptides that have been covalently modified to include one or more water soluble polymer attachments such as polyethylene glycol, polyoxyethylene glycol, or polypropylene glycol.

In a related embodiment, the present invention provides compositions comprising purified polypeptides of the invention. Preferred compositions comprise, in addition to the polypeptide of the invention, a pharmaceutically acceptable (*i.e.*, sterile and non-toxic) liquid, semisolid, or solid diluents that serve as pharmaceutical vehicles, excipients, or media. Any diluent known in the art may be used. Exemplary diluents include, but are not limited to, water, saline solutions, polyoxyethylene sorbitan monolaurate, magnesium stearate, methyl- and propylhydroxybenzoate, talc, alginates, starches, lactose, sucrose, dextrose, sorbitol, mannitol, glycerol, calcium phosphate, mineral oil, and cocoa butter.

Also comprehended by the present invention are antibodies (*e.g.*, monoclonal and polyclonal antibodies, single chain antibodies, chimeric antibodies, bifunctional/bispecific antibodies, humanized antibodies, human antibodies, and complementary determining region (CDR)-grafted antibodies, including compounds which include CDR sequences which specifically recognize a polypeptide of the invention) specific for GPCR polypeptides of the invention or fragments thereof. Preferred antibodies of the invention are human antibodies which can be produced and identified according to methods described in WO93/11236, published June 20, 1993, which is incorporated herein by reference in its entirety. Antibody fragments, including Fab, Fab', F(ab')₂, and F_w, are also provided by the invention. The term

“specific for,” when used to describe antibodies of the invention, indicates that the variable regions of the antibodies of the invention recognize and bind GPCR polypeptides exclusively (*i.e.*, able to distinguish GPCR polypeptides from other known GPCR polypeptides by virtue of measurable differences in binding affinity, despite the possible existence of localized sequence identity, homology, or similarity between GPCR polypeptides and such polypeptides). It will be understood that specific antibodies may also interact with other proteins (for example, *S. aureus* protein A or other antibodies in ELISA techniques) through interactions with sequences outside the variable region of the antibodies, and in particular, in the constant region of the molecule. Screening assays to determine binding specificity of an antibody of the invention are well known and routinely practiced in the art. For a comprehensive discussion of such assays, see Harlow *et al.* (Eds), *Antibodies A Laboratory Manual*; Cold Spring Harbor Laboratory; Cold Spring Harbor, NY (1988), Chapter 6. Antibodies that recognize and bind fragments of the GPCR polypeptides of the invention are also contemplated, provided that the antibodies are, first and foremost, specific for GPCR polypeptides. Antibodies of the invention can be produced using any method well known and routinely practiced in the art.

Non-human antibodies may be humanized by any methods known in the art. In one method, the non-human CDRs are inserted into a human antibody or consensus antibody framework sequence. Further changes can then be introduced into the antibody framework to modulate affinity or immunogenicity.

Antibodies of the invention are useful for, for example, therapeutic purposes (by modulating activity of GPCR polypeptides), diagnostic purposes to detect or quantitate GPCR polypeptides, as well as purification of GPCR polypeptides. Kits comprising an antibody of the invention for any of the purposes described herein are also comprehended. In general, a kit of the invention also includes a control antigen for which the antibody is immunospecific.

Specific binding molecules, including natural ligands and synthetic compounds, can be identified or developed using isolated or recombinant GPCR polypeptide products, GPCR polypeptide variants, or preferably, cells expressing such products. Binding partners are useful for purifying GPCR polypeptide products and

detection or quantification of GPCR polypeptide products in fluid and tissue samples using known immunological procedures. Binding molecules are also manifestly useful in modulating (*i.e.*, blocking, inhibiting or stimulating) biological activities of GPCR polypeptides, especially those activities involved in signal transduction.

5 The DNA and amino acid sequence information provided by the present invention also makes possible identification of binding partner compounds with which a GPCR polypeptide or polynucleotide will interact. Methods to identify binding partner compounds include solution assays, *in vitro* assays wherein GPCR polypeptides are immobilized, and cell based assays. Identification of binding partner
10 compounds of GPCR polypeptides provides candidates for therapeutic or prophylactic intervention in pathologies associated with GPCR polypeptide normal and aberrant biological activity.

 The invention includes several assay systems for identifying GPCR polypeptide binding partners. In solution assays, methods of the invention comprise
15 the steps of (a) contacting a GPCR polypeptide with one or more candidate binding partner compounds and (b) identifying the compounds that bind to the GPCR polypeptide. Identification of the compounds that bind the GPCR polypeptide can be achieved by isolating the GPCR polypeptide/binding partner complex, and separating
20 the GPCR polypeptide from the binding partner compound. An additional step of characterizing the physical, biological, and/or biochemical properties of the binding partner compound is also comprehended in another embodiment of the invention. In one aspect, the GPCR polypeptide/binding partner complex is isolated using a
25 antibody immunospecific for either the GPCR polypeptide or the candidate binding partner compound.

 In still other embodiments, either the GPCR polypeptide or the candidate binding partner compound comprises a label or tag that facilitates its isolation, and methods of the invention to identify binding partner compounds include
30 a step of isolating the GPCR polypeptide/binding partner complex through interaction with the label or tag. An exemplary tag of this type is a poly-histidine sequence, generally around six histidine residues, that permits isolation of a compound so labeled using nickel chelation. Other labels and tags, such as the FLAG[®] tag

- 59 -

(Eastman Kodak, Rochester, NY), well known and routinely used in the art, are embraced by the invention.

In one variation of an *in vitro* assay, the invention provides a method comprising the steps of (a) contacting an immobilized GPCR polypeptide with a candidate binding partner compound and (b) detecting binding of the candidate compound to GPCR polypeptide. In an alternative embodiment, the candidate binding partner compound is immobilized and binding of GPCR polypeptide is detected. Immobilization is accomplished using any of the methods well known in the art, including covalent bonding to a support, a bead, or a chromatographic resin, as well as non-covalent, high affinity interaction such as antibody binding, or use of streptavidin/biotin binding wherein the immobilized compound includes a biotin moiety. Detection of binding can be accomplished (i) using a radioactive label on the compound that is not immobilized, (ii) using a fluorescent label on the non-immobilized compound, (iii) using an antibody immunospecific for the non-immobilized compound, (iv) using a label on the non-immobilized compound that excites a fluorescent support to which the immobilized compound is attached, as well as other techniques well known and routinely practiced in the art.

The invention also provides cell-based assays to identify binding partner compounds of a GPCR polypeptide. In one embodiment, the invention provides a method comprising the steps of contacting a GPCR polypeptide expressed on the surface of a cell with a candidate binding partner compound and detecting binding of the candidate binding partner compound to the GPCR polypeptide. In a preferred embodiment, the detection comprises detecting a calcium flux or other physiological cellular events caused by the binding of the molecule.

Agents that modulate (*i.e.*, increase, decrease, or block) GPCR polypeptide activity or expression may be identified by incubating a putative modulator with a cell expressing a GPCR polypeptide or polynucleotide and determining the effect of the putative modulator on GPCR polypeptide activity or expression. The selectivity of a compound that modulates the activity of GPCR polypeptides can be evaluated by comparing its effects on GPCR polypeptides to its effect on other G coupled-protein receptor compounds. Selective modulators may

include, for example, antibodies and other proteins, peptides, or organic molecules which specifically bind to a G coupled-protein receptor polypeptide or a G coupled-protein receptor-encoding nucleic acid. Modulators of GPCR polypeptide activity will be therapeutically useful in treatment of diseases and physiological conditions in which normal or aberrant GPCR polypeptide activity is involved.

Methods of the invention to identify modulators include variations on any of the methods described above to identify binding partner compounds, the variations including techniques wherein a binding partner compound has been identified and the binding assay is carried out in the presence and absence of a candidate modulator. A modulator is identified in those instances where binding between the GPCR polypeptide and the binding partner compound changes in the presence of the candidate modulator compared to binding in the absence of the candidate modulator compound. A modulator that increases binding between the GPCR polypeptide and the binding partner compound is described as an enhancer or activator, and a modulator that decreases binding between the GPCR polypeptide and the binding partner compound is described as an inhibitor.

The invention also comprehends high throughput screening (HTS) assays to identify compounds that interact with or inhibit biological activity (*i.e.*, inhibit enzymatic activity, binding activity, *etc.*) of a GPCR polypeptide. HTS assays permit screening of large numbers of compounds in an efficient manner. Cell-based HTS systems are contemplated to investigate GPCR receptor-ligand interaction. HTS assays are designed to identify "hits" or "lead compounds" having the desired property, from which modifications can be designed to improve the desired property. Chemical modification of the "hit" or "lead compound" is often based on an identifiable structure/activity relationship between the "hit" and the GPCR polypeptide.

Mutations in the GPCR gene that result in loss of normal function of the GPCR gene product underlie GPCR polypeptide-related human disease states. The invention comprehends gene therapy to restore activity to treat those disease states. Delivery of a functional GPCR gene to appropriate cells is effected *ex vivo*, *in situ*, or *in vivo* by use of vectors, and more particularly viral vectors (*e.g.*, adenovirus,

- 61 -

adeno-associated virus, or a retrovirus), or *ex vivo* by use of physical DNA transfer methods (e.g., liposomes or chemical treatments). See, for example, Anderson, *Nature*, supplement to vol. 392, no. 6679, pp.25-20 (1998). For additional reviews of gene therapy technology see Friedmann, *Science*, 244: 1275-1281 (1989); Verma, *Scientific American*: 68-84 (1990); and Miller, *Nature*, 357: 455-460 (1992).

Alternatively, it is contemplated that in other human disease states, preventing the expression of or inhibiting the activity of GPCR polypeptides of the invention will be useful in treating the disease states. It is contemplated that antisense therapy or gene therapy could be applied to negatively regulate the expression of GPCR polypeptides of the invention.

Additional features of the invention will be apparent from the following Examples.

EXAMPLE 1

Cloning of G Protein-Coupled Receptors

The Incyte and Genbank expressed sequence tag (EST) databases were searched with the NCBI program Blastall using either the transmembrane VI region of known dopamine receptors (leading to the identification of CON193, CON166, CON103 and CON 203) or all known GPCR's *except* olfactory and opsin receptors (leading to the identification of CON198, CON197, CON202, CON222, CON215) as query sequences, to find patterns suggestive of novel G protein-coupled receptors. Positive hits from the find-pattern program were further analyzed with the GCG program BLAST to determine which ones were the most likely candidates to encode a GPCR, using the standard (default) alignment produced by BLAST as a guide.

A. Cloning of CON193 G Protein-Coupled Receptor

A.1. Database Search Results

Searching identified Clone 3091220H1 in the Incyte database as an interesting candidate sequence. The 3091220H1 Clone was obtained and sequenced directly using an ABI377 fluorescence-based sequencer (Perkin-Elmer/Applied Biosystems Division, PE/ABD, Foster City, CA) and the ABI PRISM™ Ready

- 62 -

Dye-Deoxy Terminator kit with Taq FSTM polymerase. Each ABI cycle sequencing reaction contained about 0.5 µg of plasmid DNA. Cycle-sequencing was performed using an initial denaturation at 98°C for 1 minute, followed by 50 cycles using the following parameters: 98°C for 30 seconds, annealing at 50°C for 30 seconds, and extension at 60°C for 4 minutes. Temperature cycles and times were controlled by a Perkin-Elmer 9600 thermocycler. Extension products were purified using Centriflex™ gel filtration cartridges (Advanced Genetic Technologies Corp., Gaithersburg, MD). Each reaction product was loaded by pipette onto the column, which was then centrifuged in a swinging bucket centrifuge (Sorvall model RT6000B tabletop centrifuge) at 1500 x g for 4 minutes at room temperature. Column-purified samples were dried under vacuum for about 40 minutes and then dissolved in 5 µl of a DNA loading solution (83% deionized formamide, 8.3 mM EDTA, and 1.6 mg/ml Blue Dextran). The samples were then heated to 90°C for three minutes and loaded into the gel sample wells for sequence analysis using the ABI377 sequencer.

Sequence analysis was done by importing ABI377 files into the Sequencer program (Gene Codes, Ann Arbor, MI). Generally, sequence reads of 700 bp were obtained. Potential sequencing errors were minimized by obtaining sequence information from both DNA strands and by re-sequencing difficult areas using primers annealing at different locations until all sequencing ambiguities were removed.

From the sequence it was deduced that Clone 3091220H1 contained only an amino-terminal fragment of a putative GPCR corresponding to the third through the seventh transmembrane regions (3TM-7TM) of a GPCR. Referring to SEQ ID NO: 1, the nucleotide sequence of Clone 3091220H1 corresponds to nucleotides 404 to 1308 of what was eventually determined to be the complete sequence of a novel seven-transmembrane receptor designated CON193. A database search with this partial sequence showed a 56% match to members of the olfactory receptor gene family, *e.g.*, the gene encoding mouse odorant receptor S19.

A.2 Screening of a Genomic Phage Library to Obtain a Full-Length GPCR Clone:

The PCR technique was used to prepare a genomic fragment for use as a probe specific for the genomic CON193 Clone. Based on the complete sequence of Clone 3091220H1, two oligonucleotide primers were designed: Primer LW1282: 5'-

- 63 -

TAATACCTGCACTGCCCCAC-3' (SEQ ID NO: 21; see nucleotides 876-894 of SEQ ID NO:1) and Primer LW1283: 5'-TCTTTCCTTCTCTTCTCACTCC-3' (SEQ ID NO: 22 see nucleotides 1137-1158 of SEQ ID NO:1). These primers were designed to amplify a 283 base-pair fragment of genomic DNA containing a portion of the
5 CON193 coding region found in Clone 3091220H1 (assuming the absence of introns in this region).

Initially, a suitable human genomic library constructed in EMBL3 SP6/T7 (Clontech Laboratories) was amplified to provide the materials required for screening. Two microliters of the human genomic library (approximately 10^8 plaque-
10 forming units per milliliter; Clontech Laboratories, catalog number HL1067J) were added to 6 ml of an overnight culture of K802 cells (Clontech Laboratories), and 250 μ l aliquots were distributed into each of 24 tubes. The tubes were incubated at 37°C for 15 minutes, and then 7 ml of 0.8% agarose (*i.e.*, top agarose) at 50°C were added to each tube. After mixing, the contents of the tubes were poured onto 150 mm LB
15 plates and incubated overnight at 37°C to allow clone amplification, evident as plaque formation (typically, confluent lysis was observed rather than discrete plaques). To each plate, 5 ml of SM phage buffer (0.1 M NaCl, 8.1 μ M $\text{MgSO}_4 \cdot 7\text{H}_2\text{O}$, 50 mM Tris-HCl (pH 7.5), and 0.0001 % gelatin) was added and the top agarose was removed by scraping with a microscope slide. Top agarose slurries containing phage were then
20 placed in individual 50 ml centrifuge tubes. A drop of chloroform was added and each tube was placed in a 37°C shaker for 15 minutes, followed by centrifuging at 2,750 x g for 15 minutes. The supernatants were isolated and separately stored at 4°C as 24 stock solutions of amplified library clones.

As noted above, polymerase chain reaction (PCR) was selected as a
25 technique for screening the phage library. Each PCR reaction was done in a 20 μ l reaction volume containing 8.84 μ l H_2O , 2 μ l 10X PCR buffer II (Perkin-Elmer), 2 μ l 25 mM MgCl_2 , 0.8 μ l dNTP mixture (dATP, dCTP, dGTP, dCTP, each at 10 mM), 0.12 μ l primer LW1282 (approximately 1 μ g/ μ l), 0.12 μ l primer LW1283 (approximately 1 μ g/ μ l), 0.12 μ l AmpliTaq Gold polymerase (5 Units/ μ l, with "Units"
30 as defined by the supplier, Perkin-Elmer) and 2 μ l of phage from one of the 24 stock tubes. The PCR reaction involved 1 cycle at 95°C for 10 minutes and 80°C for 20

- 64 -

minutes, followed by 22 cycles at 95°C for 30 seconds, 72-51°C for 2 minutes (72°C for this stage of the second cycle, with a decrease of one degree for this stage in each succeeding cycle), 72°C for one minute, followed by 30 cycles at 95°C for 15 seconds, 50°C for 30 seconds, and 72°C for one minute.

5 Following PCR cycling, the contents from each reaction tube were loaded onto a 2% agarose gel and electrophoresed adjacent to known size standards to screen for PCR products of the expected size, indicative of a clone containing the 283 bp portion of Clone 3091220H1 amplified by the two selected primers. A positive signal (*i.e.*, a fragment of the expected size) was found in one of the 24 PCR
10 reactions, thereby identifying a single stock genomic library tube containing positive clones.

 From the original genomic library tube that had given a PCR product of the correct size, a 5 µl phage aliquot was used to establish a set of five serial dilutions (1/100, v/v) that were plated and incubated in the same manner as described
15 for the amplification of the phage library. Following incubation, BA85 nitrocellulose filters (Schleicher & Schuell) were placed on top of each of the plates for 1 hour to adsorb phage from the plaques that had formed in the top agarose during incubation. Each filter was then gently removed, placed phage side up in an individual petri dish, and covered with 4 ml of SM buffer for 15 minutes to elute the phage. One milliliter
20 of SM containing eluted phage was removed from each plate and used to set up a PCR reaction as described above. The plate containing the most dilute phage solution to yield a PCR product of the expected size was then subdivided using the following procedure. A BA85 filter was placed on the top agar of the plate and the medium with applied filter was physically divided into 24 sections. After one hour to allow
25 phage adsorption to the 24 filters, each filter was removed and separately incubated in 1 ml of SM buffer at room temperature for 15 minutes. Two microliters of each eluted phage solution were then used as a PCR substrate. Those plate sections yielding positive PCR results were then subdivided into 12 subsections by removing the top agar and incubating it in 200 µl of SM buffer for one hour at room
30 temperature. Again, 2 µl of the eluted phage solutions were plated and lifted using BA85 filters, and PCR reactions were repeated. The procedure for progressive

dilution of phage was continued until a single plaque was isolated. Subsequently, 10 μ l of eluted phage from that single plaque were added to 100 μ l SM and 200 μ l of K802 cells for plating in a single petri dish as described above. A total of 7 plates were inoculated in this manner. Following incubation at 37°C for 16 hours, the top agarose from each of the 7 plates was removed to recover the phage, which were used to prepare purified genomic phage DNA using the Qiagen Lambda Midi Kit.

The purified CON193 genomic phage DNA was sequenced using the ABI PRISM™ 310 Genetic Analyzer (Perkin-Elmer/Applied Biosystems) which uses advanced capillary electrophoresis technology and the ABI PRISM™ BigDye™ Terminator Cycle Sequencing Ready Reaction Kit. The cycle-sequencing reaction contained 18 μ l of H₂O, 16 μ l of BigDye™ Terminator mix, 3 μ l of genomic phage DNA (0.26 μ g/ μ l), and 3 μ l primer (25 ng/ μ l). The reaction was performed in a Perkin-Elmer 9600 thermocycler at 95°C for 5 minutes, followed by 75 cycles of 95°C for 30 seconds, 55°C for 20 seconds, and 60°C for 4 minutes. The final subclone was also sequenced using the ABI PRISM™ 310 Genetic Analyzer. The cycle-sequencing reaction contained 6 μ l of H₂O, 8 μ l of BigDye™ Terminator mix, 5 μ l of miniprep clone DNA (0.1 μ g/ μ l), and 1 μ l primer (25 ng/ μ l). The reaction was performed in a Perkin-Elmer 9600 thermocycler at 25 cycles of 96°C for 10 seconds, 50°C for 10 seconds, and 60°C for 4 minutes. The product of the PCR reaction was purified using Centriflex™ gel filtration cartridges, dried under vacuum, and dissolved in 16 μ l of Template Suppression Reagent (PE-Applied Biosystems). The samples were then incubated at 95°C for 5 minutes and placed in the 310 Genetic Analyzer. These efforts resulted in the determination of the CON193 polynucleotide sequence set forth in SEQ ID NO:1 and the deduced amino acid sequence of the encoded CON193 polypeptide which is set forth in SEQ ID NO:2.

A.3 Subcloning of the Coding Region of CON193 via PCR

Additional experiments were conducted to subclone the coding region of CON193 and place the isolated coding region into a useful vector. Two additional PCR primers were designed based on the coding region of CON193. The first PCR primer, designated Primer LW1373, has the sequence 5'-GCATAAGCTTATGCTA-ACACTGAATAAAACAG-3' (SEQ ID NO: 23), nucleotides 11-32 of which

- 66 -

correspond to nucleotides 157-178 of SEQ ID NO: 1. The second PCR primer is Primer LW1374, which has the sequence 5'-GCATCTCGAGTCACA-TGCTGTAGGATTGG-3' (SEQ ID NO: 24, nucleotides 11-30 of which correspond to the complement of nucleotides 1102-1121 of SEQ ID NO: 1. To protect against
5 exonucleolytic attack during subsequent exposure to enzymes, *e.g.*, Taq polymerase, primers were routinely synthesized with a protective run of nucleotides at the 5' end that were not necessarily complementary to the desired target.

PCR was performed in a 50 μ l reaction containing 35 μ l H₂O, 5 μ l 10X TT buffer (140 mM ammonium sulfate, 0.1% gelatin, 0.6 M Tris-tricine, pH 8.4), 5 μ l
10 15 mM MgSO₄, 2 μ l dNTP mixture (dGTP, dATP, dTTP, and dCTP, each at 10 mM), 2 μ l genomic phage DNA (0.26 μ g/ μ l), 0.3 μ l Primer LW1373 (1 μ g/ μ l), 0.3 μ l Primer LW1374 (1 μ g/ μ l), 0.4 μ l High Fidelity Taq polymerase (Boehringer Mannheim). The PCR reaction was started with 1 cycle of 94°C for 2 minutes; followed by 15 cycles at 94°C for 30 seconds, 55°C for 30 seconds, and 72°C for 1.3
15 minutes.

The contents from the PCR reaction were loaded onto a 2% agarose gel, fractionated and electroeluted. The DNA band of expected size was excised from the gel, placed in a GenElute Agarose spin column (Supelco) and spun for 10 minutes at maximum speed in a microcentrifuge. The eluted DNA was precipitated with
20 ethanol and resuspended in 6 μ l H₂O for ligation.

The PCR-amplified DNA fragment containing the CON193 coding region was cloned into pCR2.1 using a protocol standard in the art. In particular, the ligation reaction consisted of 6 μ l of CON193 DNA, 1 μ l 10X ligation buffer, 2 μ l pCR2.1 (25 ng/ μ l, Invitrogen), and 1 μ l T4 DNA ligase (Invitrogen). The reaction
25 mixture was incubated overnight at 14°C and the reaction was then stopped by heating at 65°C for 10 minutes. Two microliters of the ligation reaction were transformed into One Shot cells (Invitrogen) and plated onto ampicillin plates. A single colony containing an insert was used to inoculate a 5 ml culture of LB medium. The culture was grown for 18 hours and the plasmid DNA was purified using the Concert Rapid Plasmid Miniprep System (GibcoBRL) and sequenced. Following confirmation of the
30 sequence, pCR-CON193 was identified, and a 50 ml culture of LB medium was

- 67 -

inoculated and recombinant plasmid DNA was purified using a Qiagen Plasmid Midi Kit to yield purified pCR-CON193.

B. Cloning of CON166 G Protein-Coupled Receptor

5 B.1 Database Search Results

The database searching identified clone 2553280H1 in the Incyte database as an interesting candidate sequence. The 2553280H1 clone was obtained and sequenced directly using an ABI377 fluorescence-based sequencer and the ABI PRISM™ Ready Dye-Deoxy Terminator kit with Taq FSTM polymerase as described
10 above for CON 193 in Example 1A.1. From the sequence it was deduced that clone 2553280H1 contained 349 nucleotides of a GPCR coding region comprising a carboxy-terminal fragment of a putative GPCR corresponding to the sixth and seventh transmembrane regions (6TM and 7TM). In addition, clone 2553280H1 contained 1.2 kb of the 3' untranslated sequence of that GPCR. Referring to SEQ ID NO: 3, the
15 nucleotide sequence of Clone 2553280H1 corresponds to nucleotides 663 to 1,014 of what was eventually determined to be the complete sequence of a novel seven-transmembrane receptor that was designated CON166. A database search with this partial sequence showed a 44% match to an activated T cell-specific G protein-coupled receptor.

20 B2. Screening of a Genomic Phage Library to Obtain a Full-Length GPCR Clone

The PCR technique was used to prepare a genomic fragment for use as a probe specific for the genomic CON166 clone. Based on the complete sequence of clone 2553280H1, two oligonucleotide primers were designed: Primer LW1278: 5'-
25 ACCGCTGCCTTTT TAGTC-3' (SEQ ID NO: 28; see nucleotides 715 to 732 of SEQ ID NO: 3 and Primer LW1279: 5'-CCTTCTTCTGGGTACATAAGTC-3' (SEQ ID NO: 29; see the reverse complement of nucleotides 951-973 of SEQ ID NO: 3). These primers were designed to amplify a 259 base-pair fragment of genomic DNA containing a portion of the CON166 coding region found in clone 2553280H1
30 (assuming the absence of introns in this region).

Initially, a suitable human genomic library constructed in EMBL SP6/T7 was amplified to provide the materials required for screening as described

- 68 -

above for CON193 in Example 1A.2. Polymerase chain reaction (PCR) was selected as a technique for screening the phage library. Each PCR reaction was done in a 20 μ l reaction volume containing 8.84 μ l H₂O, 2 μ l 10X PCR buffer II (Perkin-Elmer), 2 μ l 25 mM MgCl₂, 0.8 μ l dNTP mixture (dATP, dCTP, dGTP, dCTP, each at 10 mM),
5 0.12 μ l primer LW1278 (approximately 1 μ g/ μ l), 0.12 μ l primer LW1279 (approximately 1 μ g/ μ l), 0.12 μ l AmpliTaq Gold polymerase (5 Units/ μ l, with "Units" as defined by the supplier, Perkin-Elmer) and 2 μ l of phage from one of the 24 stock tubes. The PCR reaction involved 1 cycle at 95°C for 10 minutes and 80°C for 20 minutes, followed by 12 cycles at 95°C for 30 seconds, 72-61°C for 2 minutes (72°C
10 for this stage of the second cycle, with a decrease of one degree for this stage in each succeeding cycle), 72°C for 30 seconds, followed by 30 cycles at 95°C for 15 seconds, 60°C for 30 seconds, and 72°C for 30 seconds.

Following PCR cycling, the contents from each reaction tube were loaded onto a 2% agarose gel and electrophoresed adjacent to known size standards to
15 screen for PCR products of the expected size of 259 bp, indicative of a clone containing the portion of clone 2553280H1 amplified by the two selected primers. A positive signal (*i.e.*, a fragment of the expected size) was found in one of the 24 PCR reactions, thereby identifying a single stock genomic library tube containing positive clones.

20 From the original genomic library tube that had given a PCR product of the correct size, a 5 μ l phage aliquot was used to amplify the CON166 genomic phage DNA as described for CON 193 above in Example 1A.2. For the amplification of the phage library, the plates containing the diluted phage solution were subdivided into 12 sections unlike that of CON193; otherwise the procedures were identical.

25 The purified CON166 genomic phage DNA was sequenced using the ABI PRISM™ 310 Genetic Analyzer which uses advanced capillary electrophoresis technology and the ABI PRISM™ BigDye™ Terminator Cycle Sequencing Ready Reaction Kit as described above for CON193 in Example 1A.2. These efforts resulted in the determination of the CON166 polynucleotide sequence set forth in
30 SEQ ID NO: 3 and the deduced amino acid sequence of the encoded CON166 polypeptide which is set forth in SEQ ID NO: 4.

B.3 Subcloning of the Coding Region of CON166 via PCR

Additional experiments were conducted to subclone the coding region of CON166 from the genomic clone and place the isolated coding region into a useful vector. Two additional PCR primers were designed based on the coding region of CON166. The first PCR primer, designated Primer LW1405, has the sequence 5'-AAGCATAACATGGATGAAACAGGAAATCTG-3' (SEQ ID NO: 29, nucleotides 10-30 of which correspond to nucleotides 1-21 of SEQ ID NO: 3). To protect against exonucleolytic attack during subsequent exposure to enzymes, *e.g.*, Taq polymerase, primers were routinely synthesized with a protective run of nucleotides at the 5' end that were not necessarily complementary to the desired target. The second PCR primer is Primer LW1406, which has the sequence 5'-AAGCATAACTATACTTTACATATTTCTTC-3' (SEQ ID NO: 30, nucleotides 9-29 of which correspond to the reverse complement of nucleotides 994-1014 of SEQ ID NO: 3).

PCR was performed in a 50 μ l reaction containing 34 μ l H₂O, 5 μ l 10X TT buffer (140 mM ammonium sulfate, 0.1% gelatin, 0.6 M Tris-tricine, pH 8.4), 5 μ l 15 mM MgSO₄, 2 μ l dNTP mixture (dGTP, dATP, dTTP, and dCTP, each at 10 mM), 3 μ l genomic phage DNA (0.25 μ g/ μ l), 0.3 μ l Primer LW1405 (1 μ g/ μ l), 0.3 μ l Primer LW1406 (1 μ g/ μ l), 0.4 μ l High Fidelity Taq polymerase (Boehringer Mannheim). The PCR reaction was started with 1 cycle of 94°C for 2 minutes; followed by 25 cycles at 94°C for 30 seconds, 55°C for 30 seconds, and 72°C for 1.3 minutes.

The contents from the PCR reaction were loaded onto a 2% agarose gel and fractionated. The DNA band of expected size (1,031 bp) was excised from the gel, placed in a GenElute Agarose spin column (Supelco) and spun for 10 minutes at maximum speed in a microfuge. The eluted DNA was precipitated with ethanol and resuspended in 6 μ l H₂O for ligation.

The PCR-amplified DNA fragment containing the CON166 coding region was cloned into pCR2.1 to generate pCR-CON166 using a protocol standard in the art. In particular, the ligation reaction was carried out as described for CON193 in Example 1A.3. The resulting plasmid DNA was purified using the Concert Rapid

- 70 -

Plasmid Miniprep System (GibcoBRL) and sequenced. Following confirmation of the sequence, a 50 ml culture of LB medium was inoculated with the transformed One Shot cells, cultured, and processed using a Qiagen Plasmid Midi Kit to yield purified pCR-CON166.

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C. Cloning of CON103 G Protein-Coupled Receptor

C.1 Database Search Results

The database searching identified clone 1581220H1 in the Incyte database as an interesting candidate sequence. The 1581220H1 clone was obtained and sequenced directly using an ABI377 fluorescence-based sequencer and the ABI PRISM™ Ready Dye-Deoxy Terminator kit with Taq FSTM polymerase as described for CON 193 in Example 1A.1. From the sequence it was deduced that clone 1581220H1 contained 454 nucleotides of a GPCR coding region comprising a carboxy-terminal fragment of a putative GPCR corresponding to the sixth and seventh transmembrane regions (6TM and 7TM). In addition, clone 1581220H1 contained 1.2 kb of the 3' untranslated sequence of that GPCR. Referring to SEQ ID NO: 5, the nucleotide sequence of clone 1581220H1 corresponds to nucleotides 698 to 1190 of what was eventually determined to be the complete sequence of a novel seven-transmembrane receptor designated CON103. A database search with this partial sequence showed a 44% match to an activated T cell-specific G protein-coupled receptor.

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C.2 Screening of a Genomic Phage Library to Obtain a Full-Length GPCR Clone

The PCR technique was used to prepare a genomic fragment for use as a probe specific for the genomic CON103 clone. Based on the complete sequence of clone 1581220H1, two oligonucleotide primers were designed: Primer LW1280: 5'-TCTGCACACAGCTCTTCCATGG-3' (SEQ ID NO: 32; see nucleotides 1568-1589 of SEQ ID NO: 5) and Primer LW1281: 5'-TCCCTTGTCCAGTTGGTTGAGG-3' (SEQ ID NO: 33; see nucleotides 1926 to 1947 of SEQ ID NO: 5. These primers were designed to amplify a 380 base-pair fragment of genomic DNA containing a portion of the CON103 coding region found in clone 1581220H1 (assuming the absence of introns in this region).

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- 71 -

Initially, a suitable human genomic library constructed in EMBL SP6/T7 was amplified to provide the materials required for screening as described above for CON193 in Example 1A.2. Polymerase chain reaction (PCR) was selected as a technique for screening the phage library. Each PCR reaction was done in a 20 μ l reaction volume containing 8.84 μ l H₂O, 2 μ l 10X PCR buffer II (Perkin-Elmer), 2 μ l 25 mM MgCl₂, 0.8 μ l dNTP mixture (dATP, dTTP, dGTP, dCTP, each at 10 mM), 0.12 μ l primer LW1280 (approximately 1 μ g/ μ l), 0.12 μ l primer LW1281 (approximately 1 μ g/ μ l), 0.12 μ l AmpliTaq Gold polymerase (5 Units/ μ l, with "Units" as defined by the supplier, Perkin-Elmer) and 2 μ l of phage from one of the 24 stock tubes. PCR amplification reactions using each one of the other 23 stock collections of genomic clones were performed under the same conditions. The PCR reaction involved 1 cycle at 95°C for 10 minutes and 80°C for 20 minutes, followed by 12 cycles at 95°C for 30 seconds, 72-61°C for 2 minutes (72°C for this stage of the second cycle, with a decrease of one degree for this stage in each succeeding cycle), 72°C for one minute, followed by 30 cycles at 95°C for 15 seconds, 60°C for 30 seconds, and 72°C for 30 seconds.

Following PCR cycling, the contents from each reaction tube were loaded onto a 2% agarose gel and electrophoresed adjacent to known size standards to screen for PCR products of the expected size of 380 bp, indicative of a clone containing the portion of clone 1581220H1 amplified by the two selected primers. A positive signal (*i.e.*, a fragment of the expected size) was found in one of the 24 PCR reactions, thereby identifying a single stock genomic library tube containing positive clones.

From the original genomic library tube that had given a PCR product of the correct size, a 5 μ l phage aliquot was used to amplify the CON 103 genomic phage DNA as described above for CON193 in Example 1A.2. A total of 8 plates were inoculated with eluted phage in this manner described above. Following incubation at 37°C for 16 hours, the top agarose from each of the 8 plates was removed to recover the phage, which were used to prepare purified genomic phage DNA using the Qiagen Lambda Midi Kit.

The CON103 clone was sequenced using the ABI PRISM™ 310 Genetic Analyzer. The cycle-sequencing reaction contained 6 µl of H₂O, 8 µl of BigDye™ Terminator mix, 5 µl of miniprep clone DNA (0.1 µg/µl), and 1 µl primer (25 ng/µl). The reaction was performed in a Perkin-Elmer 9600 thermocycler at 25 cycles of 96°C for 10 seconds, 50°C for 10 seconds, and 60°C for 4 minutes. The product of the PCR reaction was purified using Centriflex™ gel filtration cartridges, dried under vacuum, and dissolved in 16 µl of Template Suppression Reagent (PE-Applied Biosystems). The samples were then incubated at 95°C for 5 minutes and placed in the 310 Genetic Analyzer. These efforts resulted in the determination of the CON103 polynucleotide sequence set forth in SEQ ID NO: 5 and the deduced amino acid sequence of the encoded CON103 polypeptide which is set forth in SEQ ID NO: 6.

C.3 Subcloning of the Coding Region of CON103 via PCR

Additional experiments were conducted to subclone the coding region of CON103 from the genomic clone and place the isolated coding region into a useful vector. Two additional PCR primers were designed based on the sequence of the coding region of CON103: Primer LW1385 (5'-GCATAAGCT-TCCATGGAAGCTTCATAACCTG-3'; SEQ ID NO: 34, nucleotides 13-30 of which correspond to nucleotides 1-18 of SEQ ID NO: 5) and Primer LW1386 (5'-GCATCTCGAGTTACCCCCACAGCGCTGCAG-3'; SEQ ID NO: 35, nucleotides 11-30 of which correspond to the reverse complement of nucleotides 1171-1190 of SEQ ID NO: 5). To protect against exonucleolytic attack during subsequent exposure to enzymes, *e.g.*, Taq polymerase, primers were routinely synthesized with a protective run of nucleotides at the 5' end that were not necessarily complementary to the desired target.

PCR was performed in a 50 µl reaction containing 22.6 µl H₂O, 5 µl 10X TT buffer (140 mM ammonium sulfate, 0.1% gelatin, 0.6 M Tris-tricine, pH 8.4), 5 µl 15 mM MgSO₄, 10 µl rapid dye (Origene), 2 µl dNTP mixture (dGTP, dATP, dTTP, and dCTP, each at 10 mM), 0.5 µl genomic phage DNA (0.97 µg/µl), 0.3 µl Primer LW1385 (1 µg/µl), 0.3 µl Primer LW1386 (1 µg/µl), and 0.4 µl High Fidelity Taq polymerase (Boehringer Mannheim). The PCR reaction was started with 1 cycle

- 73 -

of 94°C for 2 minutes, followed by 12 cycles at 94°C for 30 seconds, 55°C for 30 seconds, and 72°C for 1.3 minutes.

The contents from the PCR reaction were loaded onto a 2% agarose gel and fractionated. The DNA band of expected size (1,212 bp) was excised from the gel, placed in a GenElute Agarose spin column (Supelco) and spun for 10 minutes at maximum speed in a microcentrifuge. The eluted DNA was precipitated with ethanol and resuspended in 6 µl H₂O for ligation.

The PCR-amplified DNA fragment containing the CON103 coding region was cloned into pCR2.1 using a protocol standard in the art. In particular, the ligation reaction was carried out as described above for CON193 in Example 1A.3. The resulting plasmid DNA was purified using the Concert Rapid Plasmid Miniprep System (GibcoBRL) and sequenced. Following confirmation of the sequence, pCR-CON103 was identified, and a 50 ml culture of LB medium was inoculated, cultured, and processed using a Qiagen Plasmid Midi Kit to yield purified pCR-CON103.

D. Cloning of CON203 G Protein-Coupled Receptor

D.1 Database Search Results

The database searching identified clone 3210396H1 in the Incyte database as an interesting candidate sequence. The 3210396H1 clone was obtained and sequenced directly using an ABI377 fluorescence-based sequencer and the ABI PRISM™ Ready Dye-Deoxy Terminator kit with Taq FSTM polymerase as described above for CON193 in Example 1A.1. From the sequence it was deduced that clone 3210396H1 contained all 1,002 nucleotides of a GPCR coding region (see SEQ ID NO: 7). A database search with this sequence showed a 33% match to a platelet activating receptor (Gene H963, GenBank Acc. No. AF002986).

D.2 Subcloning of the Coding Region of CON203 via PCR

Additional experiments were conducted to subclone the coding region of CON203 and place the isolated coding region into a useful vector. Two additional PCR primers were designed based on the sequence of the coding region of CON203: Primer LW1329: 5'-GCATCTCGAGTCAGCCTAAGGTTATGTTG-3' (SEQ ID NO: 36; see nucleotides 984 to 1,002 of SEQ ID NO: 7 for the reverse complement of

- 74 -

nucleotides 9-29 of SEQ ID NO: 36) and Primer LW1377: 5'-

GCATAAGCTTATGAACACCACAGTGATGC-3' (SEQ ID NO: 37; see

nucleotides 1-19 of SEQ ID NO: 7 which correspond to nucleotides 11-29 of SEQ ID NO: 37). To protect against exonucleolytic attack during subsequent exposure to

5 enzymes, *e.g.*, Taq polymerase, primers were routinely synthesized with a protective run of nucleotides at the 5' end that were not necessarily complementary to the desired target. These primers were designed to amplify a 1,020 base-pair fragment of clone 3210396H1 containing the complete coding region of CON203.

10 PCR was performed in a 50 μ l reaction containing 34 μ l H₂O, 5 μ l 10X TT buffer (140 mM ammonium sulfate, 0.1% gelatin, 0.6 M Tris-tricine, pH 8.4), 5 μ l 15 mM MgSO₄, 2 μ l dNTP mixture (dGTP, dATP, dTTP, and dCTP, each at 10 mM), 3 μ l clone 3210396H1 (miniprep DNA), 0.3 μ l Primer LW1329 (1 μ g/ μ l), 0.3 μ l Primer LW1377 (1 μ g/ μ l), and 0.4 μ l High Fidelity Taq polymerase (Boehringer Mannheim). The PCR reaction was started with 1 cycle of 94°C for 2 minutes, 15 followed by 12 cycles at 94°C for 30 seconds, 55°C for 30 seconds, and 72°C for 1.3 minutes.

The contents from the PCR reaction were loaded onto a 1.2% agarose gel and fractionated. The DNA band of expected size (1,020 bp) was excised from the gel, placed in a GenElute Agarose spin column (Supelco) and spun for 10 minutes 20 at maximum speed in a microcentrifuge. The eluted DNA was precipitated with ethanol and resuspended in 6 μ l H₂O for ligation.

The PCR-amplified DNA fragment containing the CON203 coding region was cloned into pCR2.1 using a standard protocol and the Original TA Cloning Kit (Invitrogen). Ligation reactions were carried out as described above for CON193 25 in Example 1A.3. The resulting plasmid DNA was purified using the Concert Rapid Plasmid Miniprep System (GibcoBRL) and sequenced. Following confirmation of the sequence, pCR-C203 was identified, and a 50 ml culture of LB medium was inoculated, cultured, and processed using a Qiagen Plasmid Midi Kit to yield purified pCR-C203.

30 The CON203 clone was sequenced using the ABI PRISM™ 310 Genetic Analyzer (P-E Applied Biosystems), which uses advanced capillary

- 75 -

electrophoresis technology and the ABI Prism™ BigDye™ Terminator Cycle Sequencing Ready Reaction Kit. The cycle-sequencing reaction contained 6 µl of H₂O, 8 µl of BigDye™ Terminator mix, 5 µl of miniprep clone DNA (0.1 µg/µl), and 1 µl primer (25 ng/µl). The reaction was performed in a Perkin-Elmer 9600 thermocycler using the following conditions: 25 cycles of 96°C for 10 seconds, 50°C for 10 seconds, and 60°C for 4 minutes. The product of the PCR reaction was purified using Centriflex™ gel filtration cartridges, dried under vacuum, and dissolved in 16 µl of Template Suppression Reagent (PE-Applied Biosystems). The samples were then incubated at 95°C for 5 minutes and placed in the 310 Genetic Analyzer.

Initially, these efforts showed that the CON203 coding region cloned into pCR2.1 had a single bp difference from the corresponding sequence of clone 3210396H1. The single bp change in the pCR2.1 clone was eliminated by conforming that sequence to the sequence of clone 3210396H1 using the QuikChange Site-Directed Mutagenesis Kit (Stratagene). The method involves modification of a sequence during PCR amplification, for which PCR primers LW1387 (5'-GAGAAATATTTTCTAAAAAACCTGTTTTTGCAAAAACGG-3'; SEQ ID NO: 38) and LW1388 (5'-CCGTTTTTGCAAAAACAGGTTTTTTAGAAAA-ATATTTCTC-3'; SEQ ID NO: 39) were used. The PCR reaction contained 40 µl H₂O, 5 µl 10X proprietary Reaction Buffer (Stratagene), 1 µl pCR-C203 (0.125 µg/µl) mini-prep DNA, 1 µl dNTP mixture (dGTP, dATP, dTTP, and dCTP, each at 10 mM), 1 µl Pfu DNA polymerase (2.5 Units/µl), 1 µl LW1387 (125 ng/µl) and 1 µl LW1388 (125 ng/ l). The cycle conditions were 95°C for 30 seconds, followed by 12 cycles at 95°C for 30 seconds, 55°C for 1 minute, and 68°C for 12 minutes. The tube was then placed on ice for 2 minutes and 1 µl of *DpnI* was added. The tube was then incubated at 37°C for one hour. One microliter of the *DpnI*-treated DNA was transformed into Epicurian coli XL1-Blue supercompetent *E. coli* cells. Following isolation of pCR-C203, the entire insert was re-sequenced, thereby successfully verifying repair of the single-site polymorphism. As expected, the sequence of the CON203 coding region determined using this pCR2.1 clone is in complete agreement

- 76 -

with the CON203 coding region sequence of SEQ ID NO: 7 which specifies the amino acid sequence set forth in SEQ ID NO: 8.

E. Cloning of CON198 G Protein-Coupled Receptor

5 E.1 Database Search Results

The database searching identified Clone 3359808HI in the Incyte database as an interesting candidate sequence. The 3359808HI clone was obtained and sequenced using standard techniques. From the sequence it was deduced that Clone 3359808HI contained the entire coding region for a previously unidentified
10 GPCR, which was designated "CON198." The DNA and deduced amino acid sequences for CON198 are set forth in SEQ ID NOS: 9 and 10, respectively. A database search with this CON198 DNA sequence showed a 61% match to the rat putative GPCR designated RA1c [Raming *et. al.*, *Recept Channels*, 6: 141-151 (1998)] and 46% identity to an olfactory receptor.

15 E.2 Subcloning of the Coding Region of CON198 via PCR

Additional experiments were conducted to subclone the coding region of the CON198 clone into a useful vector. Two PCR primers were designed based on the coding region of CON198 for the purpose of PCR amplification of the CON198 coding sequence. The first, Primer LW1326, from 5' to 3' (SEQ ID NO: 42):
20 GCATGAATTCATGATGGTGGATCCCAATGG, includes the 5' end of the CON198 coding sequence (underlined) as well as a *EcoRI* restriction site, useful for subsequent expression work. The second, Primer LW1327, from 5' to 3' (SEQ ID NO: 43): GCATCTCGAGCCTAGGGCTCTGAAGCG, includes sequence complementary to the 3' end of the CON198 coding sequence (underlined), preceded
25 by a *XhoI* restriction site sequence useful for subsequent cloning and expression work.

The PCR was performed in a 50 µl reaction containing 34 µl H₂O, 5 µl of 10X TT buffer (140 mM Ammonium Sulfate, 0.1% gelatin, 0.6 M Tris-tricine, pH 8.4), 5 µl of 15 mM MgSO₄, 2 µl of 10 mM dNTPs (dATP, dCTP, dTTP, dGTP), 2 µl of Clone 3359808HI mini-prep DNA (approx. 0.125 µg/µl), 0.3 µl of Primer
30 LW1326 (1 µg/µl), 0.3 µl of Primer LW1327 (1 µg/µl), and 0.5 µl of High Fidelity Taq polymerase (Boehringer Mannheim). The PCR reaction was started with 1 cycle

- 77 -

of 94°C for 2 minutes; followed by 12 cycles at 94°C for 30 seconds, 55°C for 30 seconds, and 72°C for 1 minute.

5 The contents from the PCR reaction were loaded onto a 1.2% agarose gel and electrophoresed. The DNA band of expected size was excised from the gel, placed in a GenElute Agarose spin column (Supelco) and spun for 10 minutes at maximum speed in a microcentrifuge. The eluted DNA was ethanol-precipitated and resuspended in 6 µl H₂O for ligation.

10 The purified PCR fragment containing the CON198 coding sequence was ligated into a commercial vector using Invitrogen's Original TA Cloning Kit. The ligation reaction was carried out as described above for CON193 in Example 1A.3. The resulting plasmid DNA was isolated using a Concert Rapid Plasmid Miniprep System (GibcoBRL) and sequenced to confirm that the plasmid contained the CON198 insert. Sequencing of the subcloned CON198 construct revealed that the PCR amplification had introduced a mutation (relative to the sequence of the original
15 clone) at the nucleotide corresponding to position 204 of SEQ ID NO: 9. A site-directed mutagenesis experiment was performed using the QuikChange Site-Directed Mutagenesis Kit (Stratagene) to repair the mutation.

Two primers were designed to revert the mutated A nucleotide at position 204 back to a G nucleotide via polymerase chain reaction. Primer LW1415
20 (SEQ ID NO: 44) contained the sequence:

5'-CCATGTATATATTTCTTTGCATGCTTTCAGGCATTGACATCC-3'; and primer LW1416 (SEQ ID NO: 45) contained the sequence:

5'-GGATGTCAATGCCTGAAAGCATGCAAAGAAATATATACATGG-3'. The PCR reaction contained 40 µl of H₂O, 5 µl of 10x Reaction buffer, 1 µl of mini-prep
25 DNA (approx. 0.125 µg/µl) from the CON198-pCR2.1 clone (as template), 1 µl of primer LW1415 (125 ng/µl), 1 µl of primer LW1416 (125 ng/µl), 1 µl of 10 mM dNTPs, 1 µl Pfu DNA polymerase. The PCR cycle conditions were as follows: initial denaturation at 95°C for 30 seconds, then 14 cycles at 95°C for 30 seconds, 55°C annealing for 1 minute, and 68°C extension for 12 minutes. Thereafter, the reaction
30 tube was placed on ice for 2 minutes.

- 78 -

After PCR, 1 μ l of *DpnI* was added and the tube incubated at 37°C for one hour to digest the methylated parental DNA template. One microliter of the *DpnI*-treated DNA was transformed into Epicurian coli XL1-Blue supercompetent cells and the entire insert was re-sequenced. The resequencing confirmed that position 204 of SEQ ID NO: 9 had been successfully reverted to a guanine nucleotide.

Upon confirmation of the insert, the *E. coli* transformant was used to inoculate a 50 ml culture of LB medium. The culture was grown for 16 hours at 37°C, and centrifuged into a cell pellet. Plasmid DNA was purified from the pellet using a Qiagen Plasmid Midi Kit and again sequenced to confirm successful cloning of the CON198 insert, using an ABI377 fluorescence-based sequencer and the ABI PRISM™ Ready Dye-Deoxy Terminator kit with Taq FS™ polymerase as described above for CON 193 in Example 1A.1.

F. Cloning of CON197 G Protein-Coupled Receptor

F.1 Database Search Results

The database searching identified Clone 866390H1 in the Incyte database as an interesting candidate sequence. The 866390H1 clone was obtained and sequenced using standard techniques. From the sequence it was deduced that Clone 866390H1 contained the entire coding region for a previously unidentified GPCR, which was designated "CON197." The DNA and deduced amino acid sequences for CON197 are set forth in SEQ ID NOs: 11 and 12, respectively. A database search with this CON197 DNA sequence showed a 42% match to an olfactory receptor.

F.2 Subcloning of the Coding Region of CON197 via PCR

Additional experiments were conducted to subclone the coding region of the CON197 clone into a useful vector. Two PCR primers were designed based on the coding region of CON197 for the purpose of PCR amplification of the CON197 coding sequence. The first, Primer LW1324, from 5' to 3' (SEQ ID NO: 48): GATCGGATCCATGGAAAGCGAGAACAG, includes the 5' end of the CON197 coding sequence (underlined) as well as a *Bam*HI restriction site, useful for subsequent expression work. The second, Primer LW1325, from 5' to 3' (SEQ ID NO: 49): GATCCTCGAGTCAGGCTATGTGCTTATTAAACACC, includes

- 79 -

sequence complementary to the 3' end of the CON197 coding sequence (underlined), preceded by a *Xho*I restriction site sequence useful for subsequent cloning and expression work.

The PCR was performed in a 50 µl reaction containing 24 µl H₂O,
5 10 µl Rapid Dye Loading buffer (Origene) 5 µl 10X TT buffer (140 mM Ammonium Sulfate, 0.1% gelatin, 0.6 M Tris-tricine, pH 8.4), 5 µl of 15 mM MgSO₄, 2 µl of 10 mM dNTPs (dATP, dCTP, dTTP, dGTP), 3 µl of Clone 866390H1 mini-prep DNA (approx. 0.125 µg/µl), 0.3 µl of Primer LW1324 (1 µg/µl), 0.3 µl of Primer LW1325 (1 µg/µl), and 0.5 µl of High Fidelity Taq polymerase (Boehringer Mannheim). The
10 PCR reaction was started with 1 cycle of 94°C for 2 minutes; followed by 12 cycles at 94°C for 30 seconds, 55°C for 30 seconds, and 72°C for 1 minute.

The contents from the PCR reaction was loaded onto a 1.2% agarose gel and electrophoresed. The DNA band of expected size was excised from the gel, placed in GenElute Agarose spin column (Supelco) and spun for 10 minutes at
15 maximum speed in a Savant microcentrifuge. The eluted DNA was ethanol-precipitated and resuspended in 6 µl H₂O for ligation.

The purified PCR fragment containing the CON197 coding sequence was ligated into a commercial vector using Invitrogen's Original TA Cloning Kit. The resulting plasmid DNA from the culture was isolated using a Concert Rapid Plasmid
20 Miniprep System (GibcoBRL) and sequenced to confirm that the plasmid contained the CON197 insert.

Upon confirmation of the insert, the same transformant was used to inoculate a 50 ml culture of LB medium. The culture was grown for 16 hours at 37°C, and centrifuged into a cell pellet. Plasmid DNA was purified from the pellet
25 using a Qiagen Plasmid Midi Kit and again sequenced to confirm successful cloning of the CON197 insert, using an ABI377 fluorescence-based sequencer (Perkin Elmer/Applied Biosystems Division, PE/ABD, Foster City, CA) and the ABI PRISM™ Ready Dye-Deoxy Terminator kit with Taq FS™ polymerase as described above for CON193 in Example 1A.1.

- 80 -

G. Cloning of CON202 G Protein-Coupled Receptor

G.1 Database Search Results

The database searching identified Clone Number 1305513H1 in the Incyte database as an interesting candidate sequence. The 1305513H1 clone was obtained and sequenced using an ABI377 fluorescence-based sequencer (Perkin Elmer/Applied Biosystems Division, PE/ABD, Foster City, CA) and the ABI PRISM™ Ready Dye-Deoxy Terminator kit with Taq FS™ polymerase as described above for CON193 in Example 1A.1.

Sequencing of Incyte Clone 1305513H1 revealed a sequence corresponding to nucleotides 1054 to 1378 of SEQ ID NO: 13. Using a FORTRAN computer program called "tmrest.all" [Parodi *et al.*, *Comput. Appl. Biosci.*, 5: 527-535 (1994)], Clone 1305513H1 was deduced to contain two transmembrane-spanning domains (TMVI and TMVII) and an extracellular loop for a previously unidentified GPCR, which was designated as "CON202". The sequence obtained was used as a tool to identify a full length GPCR clone as described in the next section.

G.2 PCR Screening of Genomic Clones

A human genomic phage library was selected as a source from which to attempt to clone the CON202 gene. The genomic library was amplified as described above for CON193 in Example 1A.2.

This genomic library was screened by PCR using the primers: GV599 (5'GGCAGAAGAAGGCTATTGGTCTTAGACGAG3'; SEQ ID NO: 52), and GV600 (5'CTGAAACAGCGCCTCAGCTCCC3'; SEQ ID NO: 53). These primers were designed from the sequence of Clone 1305513H1 to amplify a 253 base pair fragment (corresponding to nucleotides 1064 to 1317 of SEQ ID NO: 13) from any corresponding genomic clone in the library. The 20 µl PCR reactions each contained 12.8 µl of H₂O, 2 µl of 10x PCR buffer II (Perkin-Elmer), 2 µl of 25 mM MgCl₂, 0.8 µl of 10 mM dNTP's (dATP, dGTP, dCTP, dTTP), 0.12 µl of primer GV599 (1 µg/ml), 0.12 µl of primer GV600 (1 µg/ml), 0.2 µl AmpliTaq Gold polymerase (5 Units/µl, with "Units" as defined by the supplier, Perkin Elmer) and 2 µl of phage from one of the 24 tubes. The PCR reaction consisted of 1 cycle at 95°C for 10 minutes; then 17 cycles at 95°C for 20 seconds, 72°C for 2 minutes decreasing 1°C

- 81 -

each cycle, 72°C for 30 seconds followed by 30 cycles at 95°C for 20 seconds, 55°C for 30 seconds, and 72°C for 30 seconds.

The PCR products were visualized on a 2% agarose gel. For those tubes which produced the correct sized band of 253 bp, five microliters from each original phage culture tube were used to amplify the CON202 genomic phage DNA as described above for CON 193 in Example 1A.2.

The genomic DNA from the single phage isolate, was sequenced with the ABI PRISM™ 310 Genetic Analyzer (PE Applied Biosystems) which uses advanced capillary electrophoresis technology and the ABI PRISM™ Big Dye™ Terminator Cycle Sequencing Ready Reaction Kit. The cycle-sequencing reaction contained 20 ml of H₂O, 16 ml of BigDye™ Terminator Mix, 1 ml of genomic phage DNA (1.1 mg/ml), and 3 ml primer (25 ng/ml). The reaction was performed in a Perkin-Elmer 9600 thermocycler at 95°C for 5 minutes, followed by 99 cycles of 95°C for 30 seconds, 55°C for 20 seconds and 60°C for 4 minutes. The product was purified using a Centriflex™ gel filtration cartridge, dried under a vacuum, then dissolved in 16 ml of Template Suppression Reagent. The samples were heated at 95°C for 5 minutes then placed in the 310 Genetic Analyzer.

G.3 Subcloning of the Coding Region of CON202 via PCR

Additional experiments were conducted to subclone the coding region of the CON202 clone into a more useful vector. Two PCR primers were designed based on the coding region of CON202 for the purpose of PCR amplification of the CON202 coding sequence. The first, Primer LW1482 (5'AGCTATGGCGAACTATAGCCATGCAGC3'; SEQ ID NO: 54) included the 5' end of the CON202 coding sequence (underlined). The second, Primer LW148 (5'AGTCCTCATATAACACAGTAAGGTTCC3'; SEQ ID NO: 55) included the sequence complementary to the 3' end of the CON202 coding sequence (underlined).

The PCR was performed in a 50 µl reaction containing 36.5 µl of H₂O, 5 µl of 10x TT buffer (140 mM Ammonium Sulfate, 0.1% gelatin, 0.6 M Tris-tricine, pH 8.4), 5 µl of 15 mM MgSO₄, 2 µl of 10 mM dNTP's (dATP, dCTP, dTTP, dGTP), 0.5 µl of CON202 genomic phage DNA (approx. 1.1 µg/µl), 0.3 µl of Primer LW1482 (1 µg/µl), 0.3 µl of Primer LW1483 (1 µg/µl), and 0.4 µl of High Fidelity Taq

- 82 -

polymerase (Boehringer Mannheim). The PCR reaction was started with 1 cycle of 94°C for 2 minutes; followed by 12 cycles at 94°C for 30 seconds, 55°C for 30 seconds, and 72°C for 1.3 minutes.

5 The contents from the PCR reaction were loaded onto a 2.1% agarose gel and electrophoresed. The DNA band of expected size (1.1 kb) was excised from the gel, placed on a GenElute Agarose spin column (Supelco), and spun for 10 minutes at maximum speed in a microfuge. The eluted DNA was ethanol-precipitated and resuspended in 6 µl of H₂O for ligation.

10 The purified PCR fragment, containing the CON202 coding sequence, was ligated into a commercial vector using Invitrogen's Original TA Cloning Kit. The ligation reaction was carried out as described above for CON193 in Example 1A.3. The resulting plasmid DNA from the culture was isolated using a Concert Rapid Plasmid Miniprep System (GibcoBRL) and sequenced to confirm that the plasmid contained the CON202 insert. The resulting construct was denoted as pCR-CON202.

15 The final subclone was sequenced using the ABI PRISM™ 310 Genetic Analyzer (PE Applied Biosystems) which uses advanced capillary electrophoresis technology and the ABI PRISM™ Terminator Cycle Sequencing Ready Reaction Kit. The cycle-sequencing reaction contained 6 ml of H₂O, 8 ml of BigDye™ Terminator mix, 5 ml miniprep DNA (0.1 mg/ml), and 1 ml primer (25
20 ng/ml). The reaction was performed in a Perkin-Elmer 9600 thermocycler at 25 cycles of 96°C for 10 seconds, 50°C for 10 seconds, and 60°C for 4 minutes. The product was purified using Centriflex™ gel filtration cartridges, dried under vacuum, then dissolved in 16 ml of Template Suppression Reagent. The samples were heated to 95°C for 5 minutes then placed in the 310 Genetic Analyzer.

25 Upon confirmation of the insert, the same transformant was used to inoculate a 50 ml culture of LB medium. The culture was grown for 16 hours at 37°C, and centrifuged into a cell pellet. Plasmid DNA was purified from the pellet using a Qiagen Plasmid Midi Kit and again sequenced to confirm successful cloning of the CON202 insert, as described above.

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- 83 -

H. Cloning of CON222 G Protein-Coupled Receptor

H.1 Database Search Results

The database searching in the Incyte database identified Sequence Number 2488822CB1 as an interesting candidate sequence. This Incyte sequence is a consensus sequence derived by compiling multiple, shorter contiguous (apparently overlapping) partial sequences from cDNA clones. A single clone known to contain the complete consensus sequence was not available from Incyte. The following experiments were performed to clone a piece of human DNA which corresponds to the region of the theoretical Incyte Sequence Number 2488822CB that was deduced to encode a heretofore undescribed GPCR. The human DNA and protein that was eventually isolated is referred to herein as CON222.

H.2 Isolation of CON222 Genomic DNA using PCR

To isolate a clone of CON222, PCR primers were designed based on the 5' and 3' ends of the open reading frame that was identified in the Incyte Sequence Number 2488822CB1. The first primer, designated as LW1440, has the sequence 5'AAGCGGATGTTTAGACCTCTTG3' (SEQ ID NO: 60) which corresponds to nucleotides 1 to 18 of SEQ ID NO: 15 (underlined). The second primer, designated LW1441, has the sequence 5'AACAGTCATGAATAGGAATTGAG3' (SEQ ID NO: 61) which is the reverse complement of nucleotides 1173 to 1191 of SEQ ID NO: 15 (underlined).

PCR was performed in a 50 ml reaction containing 22.1 ml H₂O, 10 ml Rapid Dye Loading Buffer (Origene), 5 ml 10x TT buffer (140 mM Ammonium Sulfate, 0.1% gelatin, 0.6 M Tris-tricine pH 8.4), 5 ml 15 mM MgSO₄, 2 ml 10 mM dNTP's (dATP, dCTP, dGTP, dTTP), 5 ml human genomic DNA (0.03 mg/ml) (Clontech, Cat# 6550-1), 0.3 ml of Primer LW1440 (1 mg/ml) (SEQ ID NO: 59), 0.3 ml of LW1441 (1 mg/ml) (SEQ ID NO: 60), 0.4 ml High Fidelity Taq polymerase (Boehringer Mannheim). The PCR reaction was started with 1 cycle of 94°C for 2 minutes followed by 10 cycles at 94°C for 30 seconds, 55°C for 2 minutes, 72°C for 2 minutes then 25 cycles at 94°C for 30 seconds, 55°C for 30 seconds, and 72°C for 2 minutes. The PCR reaction was loaded onto a 1.2% agarose gel. The resulting band was not 1.2 kb in length as expected, indicating that this method was unsuccessful in

- 84 -

identifying an appropriate clone from the selected Clontech genomic DNA library containing the coding region of CON222.

A human genomic DNA phage library was selected as an alternate source from which to attempt to clone the CON222 gene. Internal primers were
5 designed to attempt to isolate from a genomic library a single phage which expresses the complete coding region. The procedure was carried out as described above for CON193 in Example 1A.2.

PCR was performed to identify a phage that contained a genomic
DNA insert which corresponds to the deduced complete coding region of Incyte
10 Sequence Number 2488822CB1 using the primers: Primer LW1442:
5'GCCATTCTGTCCACAGAAG3' (SEQ ID NO: 58; see nucleotides 391 to 410 of
SEQ ID NO: 15) and Primer LW1443: 5'TCAGTTGCTGTTATGGCAC3' (SEQ ID
NO: 59; see reverse complement of nucleotides 744 to 761 of SEQ ID NO: 15).
These primers were designed based on the deduced coding region of Incyte Sequence
15 Number 2488822CB1, to amplify a 370 bp fragment (corresponding to nucleotides
391 to 761 of SEQ ID NO: 1) from any corresponding genomic clone in the library.
The 50 µl PCR reactions each contained 32 µl of H₂O, 5 µl of 10x PCR gold buffer
(PE Applied Biosystems), 5 µl of 25 mM MgCl₂, 2 µl of 10 mM dNTP's (dATP,
dCTP, dGTP, dTTP), 0.3 µl of primer LW1442 (1 µg/ml), 0.3 µl of primer LW1443
20 (1 µg/ml), 0.4 µl AmpliTaq Gold polymerase (5 U/µl, with "Units" defined by the
supplier; PE Applied Biosystems) and 5 µl of phage isolated human genomic DNA
(0.03 µg/µl). The PCR reaction consisted of 1 cycle at 95°C for 10 minutes, then 17
cycles at 95°C for 20 seconds and 72°C for 2 minutes decreasing 1 degree each cycle,
and 72°C for 1 minute, followed by 30 cycles at 95°C for 20 seconds, 55°C for 30
25 seconds, and 72°C for 1 minute. An aliquot of the PCR reaction was loaded onto a
1.2% agarose gel and electrophoresed. Although the internal primers were designed
to produce a 370 bp PCR fragment, the resulting band was approximately 1.4 kb in
length.

The DNA band was excised from the gel, placed on GenElute Agarose
30 spin columns (Supelco) and spun for 10 minutes at maximum speed in a

- 85 -

microcentrifuge. The eluted DNA was ethanol-precipitated and resuspended in 10 μ l of H₂O and 5 μ l was used to sequence the PCR band.

The PCR fragment was sequenced with an ABI PRISM™ 310 Genetic Analyzer (PE Applied Biosystems) which uses advanced capillary electrophoresis technology and the ABI PRISM™ BigDye™ Terminator Cycle Sequencing Ready Reaction Kit. Each cycle-sequencing reaction contained 6 ml of H₂O, 8 ml of BigDye Terminator mix, 5 ml PCR fragment DNA (0.2 mg/ml), and 1 ml Primer LW1442 (25 ng/ml) and Primer LW1443 (25 ng/ml). The reaction was performed in a Perkin-Elmer 9600 thermocycler with 25 cycles of 96°C for 10 seconds, 50°C for 10 seconds, and 60°C for 4 minutes. The product was purified using Centriflex™ gel Reagent (PE Applied Biosystems). The samples were heated at 95°C for 5 minutes then placed in the 310 Genetic Analyzer.

The sequence analysis determined that there is an intron in the middle of the 5th transmembrane-spanning domain between nucleotides 673 and 674 in SEQ ID NO: 15. This intron was responsible for the unexpectedly large PCR fragment.

H.3 Isolation of Full Length cDNA

Since attempts to isolate an uninterrupted coding region from genomic DNA were unsuccessful, a fetal brain cDNA was used to generate the complete coding region of Incyte Sequence Number 2488833CB1. The PCR primers described above, LW1440 (SEQ ID NO: 60) and LW1441 (SEQ ID NO: 61), which correspond to the 5' and 3' end of CON222 respectively, were used to generate the full length coding region.

The 50 μ l PCR reaction contained 37.4 μ l of H₂O, 5 μ l of 10x cDNA PCR buffer (Clontech), 1 μ l of 10 mM dNTP's (dATP, dCTP, dTTP, dGTP), 5 μ l of Marathon-Ready Fetal Brain cDNA (Clontech), 0.3 μ l of Primer LW1440 (1 μ g/ μ l), 0.3 μ l of Primer LW1441 (1 μ g/ μ l), and 1 μ l of 50x Advantage cDNA polymerase (Clontech). The PCR reaction was started with 1 cycle of 94°C for 1 minute, followed by 30 cycles at 94°C for 30 seconds, 50°C for 30 seconds, and 68°C for 3 minutes.

The contents from the PCR reaction were loaded onto a 1.2% agarose gel and electrophoresed. The DNA band of expected size (1.2 kb) was excised from

- 86 -

the gel, placed on a GenElute Agarose spin column (Supelco), and spun for 10 minutes at maximum speed in a microfuge. The eluted DNA was ethanol-precipitated and resuspended in 6 μ l H₂O for ligation.

H.4 Subcloning of Coding Region of CON222 via PCR

5 After a cDNA containing the full length CON222 open reading frame was obtained, the coding region of CON222 was then subcloned into a more useful vector as follows.

 The purified PCR fragment described above, containing the CON222 coding sequence, was ligated into a commercial vector using Invitrogen's Original TA
10 Cloning Kit. The ligation reaction was carried out as described above for CON193 in Example 1A.3. The resulting plasmid DNA from the culture was isolated using a Concert Rapid Plasmid Miniprep System (GibcoBRL) and sequenced to confirm that the plasmid contained the CON222 insert.

 The subcloned insert in pCR2.1 was sequenced using the ABI
15 PRISM™ 310 Genetic Analyzer (PE Applied Biosystems) which uses advanced capillary technology and the ABI PRISM™ BigDye™ Terminator Cycle Sequencing Ready Reaction Kit. Each cycle-sequence reaction contained 6 ml of H₂O, 8 ml of BigDye™ Terminator mix, 5 ml mini-prep DNA (0.1 mg/ml), and 1 ml of primer (25 ng/ml) and was performed in a Perkin-Elmer 9600 thermocycler with 25 cycles of
20 96°C for 10 seconds, 50°C for 10 seconds, and 60°C for 4 minutes. The product was purified using a Centriflex™ gel filtration cartridge, vacuum dried and dissolved in 16 ml of Template Suppression Reagent (PE Applied Biosystems). The samples were heated at 95°C for 5 minutes then placed in the 310 Genetic Analyzer.

 Upon confirmation of the insert, the same transformant was used to
25 inoculate a 50 ml culture of LB medium. The culture was grown for 16 hours at 37°C, and centrifuged into a cell pellet. Plasmid DNA was purified from the pellet using a Qiagen Plasmid Midi Kit and again sequenced to confirm successful cloning of the CON222 insert, as described above.

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- 87 -

I. Cloning of CON215 G Protein-Coupled Receptor**I.1 Database Search Results**

The database searching identified Clone 1452259H1 in the Incyte database as an interesting candidate sequence. The sequence from 1452259H1 clone was used to search the Incyte full-length database and matched the entry 1650519CB1. An inspection of the clones that made up 1650519CB1 indicated that Incyte Clone 2796157H1 probably contained the full-length coding region. Sequence analysis of Incyte Clone 2796157H1 indicated that it contains the entire coding region for a previously unidentified GPCR, which was designated "CON215", along with 12 nucleotides of 5' untranslated region, 63 nucleotides of 3' untranslated region and a poly A⁺ tail. The DNA and deduced amino acid sequences for CON215 are set forth in SEQ ID NOS: 17 and 18, respectively. A database search with this CON215 sequence showed a 47% match to the human probable G protein-coupled receptor KIA0001.

Since the untranslated regions were relatively short, it was not necessary to remove the coding region of CON215 from the pINCY vector (Incyte) and the construct is referred to as pINCY-CON215. The Incyte Clone 2796157H1 was sequenced using the ABI PRISM™ 310 Genetic Analyzer (PE Applied Biosystems) which uses advanced capillary electrophoresis technology and the ABI PRISM™ BigDye™ Terminator Cycle Sequencing Ready Reaction Kit as described above for CON222 in Example 1H.4.

J. Cloning of CON217 G Protein-Coupled Receptor**J.1 Database Search Results**

The Incyte database search identified EST 3700658H1 as an interesting candidate sequence. The EST sequence No. 3700658H1 was used to search the Incyte full length database. This search identified Incyte clone No. 3356166H1 as a clone that potentially contained a full length GPCR corresponding to the selected EST.

The 3356166H1 clone was obtained from Incyte and sequenced using an ABI377 fluorescence-based sequencer (and the ABI PRISM™ Ready Dye-Deoxy

- 88 -

Terminator kit with Taq FS™ polymerase as described above for CON193 in Example 1A.1.

Sequencing of Incyte Clone No. 3356166H1 revealed a 2480 basepair sequence as shown in SEQ NO: 19. Using a FORTRAN computer program called "tmtrest.all" [Parodi *et al.*, *Comput. Appl. Biosci.*, 5: 527-535 (1994)], Clone No. 3356166H1 was deduced to contain seven transmembrane-spanning domains (TMI-TMVII) and was designated as "CON217" (SEQ ID NO: 20). The following experiments were performed to subclone and isolate the full length coding sequence of CON217 from Incyte Clone No. 3356166H1.

J.2 Subcloning of the Coding Region of GPCR217

To subclone the full length coding sequence of CON217, PCR primers were designed based on the 5' and 3' ends of the open reading frame that was identified in the Incyte Clone No. 3356166H1. The first primer, designated as LW1448, has the sequence 5'AAGCGGTACCATGTTAGCCAACAGCTCCTC3' (SEQ ID NO: 66) which corresponds to nucleotides 42 to 62 of SEQ ID NO: 19 (underlined). The second primer, designated LW1449, has the sequence 5'AAGCTCTAGATCAGAGGGCGGAATCCTGG3' (SEQ ID NO: 67) which is the reverse complement of nucleotides 1142 to 1160 of SEQ ID NO: 20 (underlined). The primers also include recognition sequences (bold) for the restriction enzymes KpnI and XbaI, respectively.

PCR was performed in a 50 ml reaction containing 32.5 ml of H₂O, 5 ml of 10x Pfx Amplification buffer (GibcoBRL), 5 ml of 10x PCR Enhancer solution (GibcoBRL), 1.5 ml of 50 mM MgSO₄, 2 ml of 10 mM dNTP's (dATP, dCTP, dGTP, dTTP), 3 ml 3356166H1 mini-prep DNA (0.125 mg/ml obtained with the Concert Rapid Plasmid Miniprep System; GibcoBRL), 0.3 ml of Primer LW1448 (1 mg/ml) (SEQ ID NO: 3), 0.3 ml of Primer LW1449 (1 mg/ml) (SEQ ID NO: 4), 0.5 ml Platinum Pfx DNA polymerase (2.5 U/ml; GibcoBRL). The PCR reaction was started with 1 cycle of 94°C for 2 minutes followed by 25 cycles at 94°C for 30 seconds, 55°C for 30 seconds, 68°C for 1.3 minutes.

The contents from the PCR reaction were loaded onto a 1.2% agarose gel and electrophoresed. The DNA band of expected size (~1.1 kb) was excised from

- 89 -

the gel, placed on a GenElute Agarose spin column (Supelco), and spun for 10 minutes at maximum speed in a microfuge. The eluted DNA was ethanol-precipitated and resuspended in 6 µl of H₂O for ligation.

5 The purified PCR fragment, containing the CON217 coding sequence, was ligated into a commercial vector designated pCR2.1 using Invitrogen's Original TA Cloning Kit. The ligation reaction was carried out as described above for CON193 in Example 1A.3. The resulting plasmid DNA from the culture was isolated using a Concert Rapid Plasmid Miniprep System (GibcoBRL) and sequenced to confirm that the plasmid contained the CON217 insert and to confirm that no errors
10 were introduced during PCR amplification. The resulting construct was denoted as pCR-CON217.

The final subclone was sequenced using the ABI PRISM™ 310 Genetic Analyzer (PE Applied Biosystems) which uses advanced capillary electrophoresis technology and the ABI PRISM™ Terminator Cycle Sequencing
15 Ready Reaction Kit as described above for CON222 in Example 1H.4.

EXAMPLE 2

Analysis of G Protein-Coupled Receptor Sequence

A. CON193

20 The DNA and deduced amino acid sequence for CON193 are set forth in SEQ ID NOS: 1 and 2, respectively. Beginning with the initiation codon (methionine), the CON193 genomic Clone contains an open reading frame of 963 nucleotides encoding 321 amino acids, followed by a stop codon. Using a FORTRAN computer program called "tmrest.all" [Parodi *et al.*, *Comput. Appl. Biosci.*, 5: 527-
25 535 (1994)], CON193 was shown to contain seven transmembrane-spanning domains corresponding to residues 30-49 (1TM), 61-81 (2TM), 103-122 (3TM), 146-165 (4TM), 199-222 (5TM), 243-262 (6TM), and 270-295 (7TM) of SEQ ID NO: 2. These transmembrane domains define first ("N-terminal," residues 1-29), second ("first EC loop," residues 82-102), third ("second EC loop," residues 166-198), and
30 fourth ("third EC loop," residues 263-269) extracellular domains, as well as first ("first IC loop," residues 50-60), second ("second IC loop," residues 123-145), third

- 90 -

("third IC loop," residues 223-242), and fourth ("C-terminal," residues 296-321) intracellular domains.

Inspection of the CON193 amino acid sequence (SEQ ID NO: 2) reveals that this GPCR contains a DRY sequence following the third transmembrane domain (3TM) and a PIVY sequence found in the sixth transmembrane domain (TM6). In addition, the CON193 polynucleotide sequence was compared to sequences of known genes. CON193 is 45% identical and 72% similar to the mouse olfactory receptor gene S19 [see Malnic et al., Cell 96:713-723 (1999)]. This level of sequence similarity suggests that CON193 is a novel GPCR.

The CON193 cDNA clone (SEQ ID NO:1) was deposited with the National Center for Agricultural Utilization Research at the United States Department of Agriculture 1815 North University Street, Peoria, Illinois 61604 in accordance with the Budapest Treaty on January 18, 2000. The clone was given accession no. B-30250.

B. CON166

The DNA and deduced amino acid sequence for CON166 are set forth in SEQ ID NOS: 3 and 4, respectively. Beginning with the initiation codon (methionine), the CON166 genomic clone contains an open reading frame of 1,011 nucleotides encoding 337 amino acids, followed by a stop codon. Using a FORTRAN computer program called "tmrest.all" [Parodi *et al.*, *Comput. Appl. Biosci.*, 5: 527-535 (1994)], CON166 was shown to contain seven transmembrane-spanning domains corresponding to the following residues presented in SEQ ID NO: 4: 1TM (30-49), 2TM (59-79), 3TM (99-119), 4TM (141-161), 5TM (191-215), 6TM (231-251), and 7TM (277-296). These transmembrane domains define first ("N-terminal," residues 1-29), second ("first EC loop," residues 80-98), third ("second EC loop," residues 162-190), and fourth ("third EC loop," residues 252-276), extracellular domains as well as first ("first IC loop," residues 50-58), second ("second IC loop," residues 120-140), third ("third IC loop," residues 216-230), and fourth ("C-terminal," residues 297-337) intracellular domains.

- 91 -

Inspection of the CON166 amino acid sequence (SEQ ID NO:2) reveals that this GPCR contains an FRC sequence following the third transmembrane domain (3TM), which is typically occupied by a consensus DRY sequence in other GPCRs; a PLLY sequence is also found in the seventh transmembrane domain (7TM).

5 In addition, the CON166 polynucleotide sequence was compared to sequences of known genes. CON166 is 44% identical and 62% similar to a T-cell-specific G protein-coupled receptor of *Gallus gallus* found in the TREMBL database (Accession No. L06109). This level of sequence similarity suggests that CON166 is a novel GPCR.

10 The CON166 cDNA clone (SEQ ID NO:3) was deposited with the National Center for Agricultural Utilization Research at the United States Department of Agriculture 1815 North University Street, Peoria, Illinois 61604 in accordance with the Budapest Treaty on January 18, 2000. The clone was given accession no. B-30248.

15 C. CON103

The DNA and deduced amino acid sequence for CON103 are set forth in SEQ ID NOS: 5 and 6, respectively. Beginning with the initiation codon (methionine), the CON103 genomic clone contains an open reading frame of 1,152
20 nucleotides encoding 384 amino acids, followed by a stop codon and a short open reading frame (SEQ ID NO: 5). Using a FORTRAN computer program called "tmrest.all" [Parodi *et al.*, *Comput. Appl. Biosci.*, 5: 527-535 (1994)], CON103 was shown to contain seven transmembrane-spanning domains corresponding to the following residues in SEQ ID NO: 6: 54-77 (1TM), 89-108 (2TM), 134-149 (3TM),
25 167-188 (4TM), 216-240 (5TM), 258-283 (6TM), and 301-320 (7TM). These transmembrane domains define first ("N-terminal," residues 1-53), second ("first EC loop," residues 109-133), third ("second EC loop," residues 189-215), and fourth ("third EC loop," residues 284-300) extracellular domains, as well as first ("first IC loop," residues 78-88), second ("second IC loop," residues 150-166), third ("third IC loop," residues 241-257), and fourth ("C-terminal," residues 321-384) intracellular
30 domains.

- 92 -

Inspection of the CON103 amino acid sequence (SEQ ID NO: 6) reveals that this GPCR contains an NRY sequence following the third transmembrane domain (3TM), which is typically occupied by a consensus DRY sequence in other GPCRs. In addition, the CON103 polynucleotide sequence was compared to sequences of known genes. CON103 is 36% identical to GPR31 (GenBank Accession No. U65402) and 31% identical to the P2Y1 purinergic receptor (GenBank Accession No. S81950). This level of sequence similarity indicates that CON103 is a novel GPCR.

The CON103 cDNA clone (SEQ ID NO:5) was deposited with the National Center for Agricultural Utilization Research at the United States Department of Agriculture 1815 North University Street, Peoria, Illinois 61604 in accordance with the Budapest Treaty on January 18, 2000. The clone was given accession no. B-30247.

D. CON203

The DNA and deduced amino acid sequence for CON203 are set forth in SEQ ID NOS: 7 and 8, respectively. Beginning with the initiation codon (methionine), the CON203 genomic clone contains an open reading frame of 999 nucleotides encoding 333 amino acids, followed by a stop codon. Using a FORTRAN computer program called "tmtest.all" [Parodi *et al.*, *Comput. Appl. Biosci.*, 5: 527-535 (1994)], CON203 was shown to contain seven transmembrane-spanning domains corresponding to the following residues of SEQ ID NO: 7: nucleotides 29-53 (1TM), 63-82 (2TM), 97-118 (3TM), 136-160 (4TM), 189-211 (5TM), 232-252 (6TM), and 281-300 (7TM). These transmembrane domains define first ("N-terminal," residues 1-28), second ("first EC loop," residues 83-96), third ("second EC loop," residues 161-188), and fourth ("third EC loop," residues 253-280) extracellular domains, as well as first ("first IC loop," residues 54-62), second ("second IC loop," residues 119-135), third ("third IC loop," residues 212-231), and fourth ("C-terminal," residues 301-333) intracellular domains.

Inspection of the CON203 amino acid sequence (SEQ ID NO: 8) reveals that this GPCR contains a DRF sequence following the third transmembrane

- 93 -

domain (3TM), which is typically occupied by a consensus DRY sequence in other GPCRs; CON203 also exhibited a PLIY sequence in the seventh transmembrane domain (7TM). In addition, the CON203 polynucleotide sequence was compared to sequences of known genes. CON203 is 33% identical to a platelet activating receptor (GenBank Accession No. AF002986. This level of sequence similarity suggests that CON203 is a novel GPCR.

The CON203 cDNA clone (SEQ ID NO: 7) was deposited with the National Center for Agricultural Utilization Research at the United States Department of Agriculture 1815 North University Street, Peoria, Illinois 61604 in accordance with the Budapest Treaty on January 18, 2000. The clone was given accession no. B-30254.

E. CON198

The DNA and deduced amino acid sequence for CON198 are set forth in SEQ ID NO: 9 and 10 respectively. Beginning with the initiator methionine, the CON198 genomic clone contains an open reading frame of 954 nucleotides encoding 318 amino acids, followed by a stop codon. It will be appreciated that residue 2 of SEQ ID NO: 10 also is a methionine. Amino-terminal sequencing of purified native or recombinant CON198 protein will provide an indication as to which methionine acts as an initiator codon *in vivo*. Using a FORTRAN computer program called "tmrest.all" [Parodi *et al.*, *Comput. Appl. Biosci.*, 5: 527-535 (1994)], CON198 was deduced to contain seven transmembrane-spanning domains corresponding to residues 28-52 (TM1), 61-80 (TM2), 104-123 (TM3), 147-167 (TM4), 200-226 (TM5), 239-263 (TM6), and 274-295 (TM7) of SEQ ID NO: 10. These transmembrane domains define first ("N-terminal," residues 1-27 or 2-27), second ("first EC loop," residues 81-103), third ("second EC loop," residues 168-199), and fourth ("third EC loop," residues 264-273) extracellular domains as well as first ("first IC loop," residues 53-60), second ("second IC loop," residues 124-146), third ("third IC loop," residues 227-238), and fourth ("C-terminal," residues 296-318) intracellular domains.

CON198 contains a DRY sequence following the third transmembrane domain (TM3), a feature that is conserved in most GPCR. The most similar sequence

- 94 -

in a public database, at the time of initial screening, was that of rat GPCR RA1c, which shared only 61% identity at the amino acid level.

The CON198 cDNA clone (SEQ ID NO: 9) was deposited with the National Center for Agricultural Utilization Research at the United States Department of Agriculture 1815 North University Street, Peoria, Illinois 61604 in accordance with the Budapest Treaty on January 18, 2000. The clone was given accession no. B-30252.

F. CON197

The DNA and deduced amino acid sequence for CON197 are set forth in SEQ ID NO: 11 and 12, respectively. Beginning with the initiator methionine, the CON197 genomic clone contains an open reading frame of 921 nucleotides encoding 307 amino acids, followed by a stop codon. Using a FORTRAN computer program called "tmrest.all" [Parodi *et al.*, *Comput. Appl. Biosci.*, 5: 527-535 (1994)], CON197 was deduced to contain seven transmembrane-spanning domains corresponding to residues 23-47 (TM1), 58-78 (TM2), 99-120 (TM3), 142-164 (TM4), 195-219 (TM5), 237-258 (TM6), and 270-289 (TM7) of SEQ ID NO: 12. These transmembrane domains define first ("N-terminal" residues 1-22), second ("first EC loop" residues 79-98), third ("second EC loop" residues 165-194), and fourth ("third EC loop" residues 259-269) extracellular domains as well as first ("first IC loop" residues 48-57), second ("second IC loop" residues 121-141), third ("third IC loop" residues 220-236), and fourth ("C-terminal" residues 290-309) intracellular domains.

CON197 contains a DRY sequence following the third transmembrane domain (TM3), a feature that is conserved in most GPCR. The most similar sequence in a public database, at the time of initial screening, was that of an olfactory receptor, which shared only 42% identity at the amino acid level.

The CON197 cDNA clone (SEQ ID NO: 11) was deposited with the National Center for Agricultural Utilization Research at the United States Department of Agriculture 1815 North University Street, Peoria, Illinois 61604 in accordance with the Budapest Treaty on January 18, 2000. The clone was given accession no. B-30251.

G. CON202

The DNA and deduced amino acid sequence for this phage insert, termed "CON202", are set forth in SEQ ID NO: 13 and 14, respectively. The CON202 open reading frame, as depicted in SEQ ID NO: 14, begins with the initiator methionine and spans 1110 nucleotides which encode 370 amino acids, followed by a stop codon. Since this gene was isolated from genomic DNA and there are no apparent interruptions in the sequence, it is likely that CON202 contains no introns within the coding region. The full length clone of CON202 contained seven transmembrane-spanning domains corresponding to residues, 24 to 46 (TM1), 57 to 77 (TM2), 96 to 117 (TM3), 135 to 159, (TM4) TMV comprises 184 to 202 (TM5), 286 to 308 (TM6), 316 to 339 (TM7) of SEQ ID NO: 14. TM2 terminates with PFVC instead of the characteristic PXXY. TM3 is followed by the sequence TRY instead of the characteristic DRY. These transmembrane domains define first ("N-terminal," residues 1-23), second ("first EC loop," residues 78-95), third ("second EC loop," residues 160-183), and fourth ("third EC loop," residues 309-315) extracellular domains as well as first ("first IC loop," residues 47-56), second ("second IC loop," residues 118-134), third ("third IC loop," residues 203-285), and fourth ("C-terminal," residues 340-370) intracellular domains.

The CON202 cDNA clone (SEQ ID NO: 13) was deposited with the National Center for Agricultural Utilization Research at the United States Department of Agriculture 1815 North University Street, Peoria, Illinois 61604 in accordance with the Budapest Treaty on January 18, 2000. The clone was given accession no. B-30253.

H. CON222

The sequence of CON222 coding region deduced the DNA and amino acid sequence set forth in SEQ ID NO: 15 and 16, respectively. The open reading frame that is depicted in SEQ ID NO: 16 begins with an initiator codon and spans 1188 nucleotides which encode 396 amino acids, followed by a stop codon.

The full length clone of CON222 contains seven transmembrane-spanning domains corresponding to residues 42-65 (TM1) 79-103, (TM2), 125-156,

- 96 -

(TM3), 167-188 (TM4), 217-241 (TM5), 268-290 (TM6), 301-320 (TM7) of SEQ ID NO: 16. TM2 is followed by a FRC sequence and TM7 contains a PILEY sequence within. These transmembrane domains define first ("N-terminal," residues 1-41), second ("first EC loop," residues 104-124), third ("second EC loop," residues 189-216), and fourth ("third EC loop," residues 291-300) extracellular domains as well as first ("first IC loop," residues 66-78), second ("second IC loop," residues 157-166), third ("third IC loop," residues 242-267), and fourth ("C-terminal," residues 321-396) intracellular domains. A search of the public database indicated that CON222 is about 35% identical to a unique GPCR found in the nervous system of *Lymnaea stagnalis*.

The CON222 cDNA clone (SEQ ID NO: 15) was deposited with the National Center for Agricultural Utilization Research at the United States Department of Agriculture 1815 North University Street, Peoria, Illinois 61604 in accordance with the Budapest Treaty on January 18, 2000. The clone was given accession no. B-30257.

I. CON215

The DNA and deduced amino acid sequence for CON215 are set forth in SEQ ID NO: 17 and 18, respectively. Beginning with the initiator methionine, the CON215 genomic clone contains an open reading frame of 1074 nucleotides encoding 358 amino acids, followed by a stop codon. Using a FORTRAN computer program called "tmrest.all" [Parodi *et al.*, *Comput. Appl. Biosci.*, 5: 527-535 (1994)], CON215 was deduced to contain seven transmembrane-spanning domains corresponding to residues 42-66 (TM1), 81-99 (TM2), 116-137 (TM3), 156-180 (TM4), 210-234 (TM5), 256-275 (TM6), and 308-328 (TM7) of SEQ ID NO: 18. These transmembrane domains define first ("N-terminal," residues 1-41), second ("first EC loop," residues 100-115), third ("second EC loop," residues 181-209), and fourth ("third EC loop," residues 276-307) extracellular domains as well as first ("first IC loop," residues 67-80), second ("second IC loop," residues 138-155), third ("third IC loop," residues 235-255), and fourth ("C-terminal," residues 329-358) intracellular domains.

- 97 -

CON215 contains a DRY sequence following the third transmembrane domain (TM3), a feature that is conserved in most GPCR. CON215 also contains a PLVY sequence within the seventh transmembrane domain (TM7).

5 The CON215 cDNA clone (SEQ ID NO: 17) was deposited with the National Center for Agricultural Utilization Research at the United States Department of Agriculture 1815 North University Street, Peoria, Illinois 61604 in accordance with the Budapest Treaty on January 18, 2000. The clone was given accession no. B-30255.

10 **J. CON217**

The DNA and deduced amino acid sequences of CON217 are set forth as SEQ ID NO: 19 and 20, respectively. The open reading frame that is depicted in SEQ ID NO: 2 begins with an initiator methionine codon and spans 1116 nucleotides which encode 372 amino acids, followed by a stop codon. In addition, the nucleotide
15 sequence consists of 41 bp in the 5' untranslated region and 1323 bp in the 3' untranslated region.

The full length clone of CON217 contains seven transmembrane-spanning domains as indicated by the FORTRAN computer program "tmrest.all" [Parodi *et al.*, *Comput. Appl. Biosci.*, 5: 527-535 (1994)] which corresponds to 29-50
20 (TM1), 57-75 (TM2), 96-117 (TM3), 137-160 (TM4), 188-210 (TM5), 235-258 (TM6), 277-297 (TM7). TM3 is followed by a DRY sequence and TM7 contains a PLVY sequence within. These transmembrane domains define first ("N-terminal," residues 1-28), second ("first EC loop," residues 76-95), third ("second EC loop," residues 161-187), and fourth ("third EC loop," residues 259-276) extracellular
25 domains as well as first ("first IC loop," residues 51-56), second ("second IC loop," residues 118-136), third ("third IC loop," residues 211-234), and fourth ("C-terminal," residues 298-372) intracellular domains. A search of the public database indicated that CON217 is about 41% identical to GPR23 (Genebank Accession No.: U66578) and to a purinergic receptor P2Y9 (Genebank Accession No.: U90322).

30 The CON215 cDNA clone (SEQ ID NO: 19) was deposited with the National Center for Agricultural Utilization Research at the United States Department

- 98 -

of Agriculture 1815 North University Street, Peoria, Illinois 61604 in accordance with the Budapest Treaty on January 18, 2000. The clone was given accession no. B-30256.

5 K. Summary of Deposits

The polynucleotides (SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15 and 17) encoding the GPCR polypeptides of the invention were deposited with the Agricultural Research Service Culture Collection (NRRL) at the National Center Agricultural Utilization Research at the U.S. Department of the Agriculture 1815 North University Street, Peoria, Illinois 61604. These deposits were made in accordance with the Budapest Treaty on the International Recognition of the Deposit of Microorganism for the Purposes of Patent Procedures. The table below lists the details of these deposits.

	<u>GPCR</u>	<u>SEQ ID NO:</u>	<u>NRRL No.</u>	<u>Deposit Date</u>
15	CON193	1	B-30250	1/18/00
	CON166	3	B-30248	1/18/00
	CON103	5	B-30247	1/18/00
	CON203	7	B-30254	1/18/00
	CON198	9	B-30252	1/18/00
20	CON197	11	B-30251	1/18/00
	CON202	13	B-30253	1/18/00
	CON222	15	B-30257	1/18/00
	CON215	17	B-30255	1/18/00
	CON217	19	B-30256	1/18/00

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EXAMPLE 3

Hybridization Analysis Demonstrates that the GPCRs are Expressed in the Brain

The expression of GPCR polynucleotides in mammals, such as the rat, was investigated by *in situ* hybridization histochemistry. Coronal and sagittal rat.

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- 99 -

brain cryosections (20 μ m thick) were prepared using a Reichert-Jung cryostat. Individual sections were thaw-mounted onto silanized, nuclease-free slides (CEL Associates, Inc., Houston, TX), and stored at -80°C. Sections were processed starting with post-fixation in cold 4% paraformaldehyde, rinsed in cold phosphate-buffered saline (PBS), acetylated using acetic anhydride in triethanolamine buffer, and dehydrated through a series of alcohol washes in 70%, 95%, and 100% alcohol at room temperature. Subsequently, sections were delipidated in chloroform, followed by rehydration through successive exposure to 100% and 95% alcohol at room temperature. Microscope slides containing processed cryosections were allowed to air dry prior to hybridization.

A. CON193

A CON193-specific probe was generated using PCR. The probe consisted of a 270 bp fragment containing sequence at the 3' end of CON-193. The primers for PCR amplification were LW 1248 [5'-GCATGAATTCCAATATACTTCCCCATACCTAC-3'; SEQ ID NO: 26) and LW 1249 [5'-GCATGGATCCGGAAAAGAAGGAGAAGAAAG-3'; SEQ ID NO: 27), which introduced terminal *Eco*RI and *Bam*HI restriction sites into the PCR product. Following PCR amplification, the fragment was digested with *Eco*RI and *Bam*HI and cloned into pBluescriptII cleaved with the same enzymes. For production of a probe specific for the sense strand of CON193, the CON193 Clone in pBluescriptII was linearized with *Bam*HI, which provided a substrate for labeled run-off transcripts (*i.e.*, cRNA riboprobes) using the vector-borne T7 promoter and commercially available T7 RNA polymerase. A probe specific for the antisense strand of CON193 was also readily prepared using the CON193 Clone in pBluescriptII by cleaving the recombinant plasmid with *Eco*RI to generate a linearized substrate for the production of labeled run-off cRNA transcripts using the T3 promoter and cognate polymerase. The riboprobes were labeled with [³⁵S]-UTP to yield a specific activity of 0.81 x 10⁶ cpm/pmol for antisense riboprobes and 0.55 x 10⁶ cpm/pmol for sense-strand riboprobes. Both riboprobes were subsequently denatured by incubating at 70°C for 3 minutes and added (2 pmol/ml) to hybridization buffer which contained 50%

- 100 -

formamide, 10% dextran, 0.3 M NaCl, 10 mM Tris (pH 8.0), 1 mM EDTA, 1X Denhardt's Solution, and 10 mM dithiothreitol. Microscope slides containing sequential brain cryosections were independently exposed to 45 μ l of hybridization solution per slide and silanized cover slips were placed over the sections being
5 exposed to hybridization solution. Sections were incubated overnight (15-18 hours) at 52°C to allow hybridization to occur. Equivalent series of cryosections were exposed to sense or antisense CON193-specific cRNA riboprobes.

Following the hybridization period, coverslips were washed off the slides in 1X SSC. Slides were subjected to RNase A treatment by incubation in a
10 buffer containing 20 μ g/ml RNase A, 10 mM Tris (pH 8.0), 0.5 M NaCl and 1 mM EDTA for 45 minutes at 37°C. The cryosections were then subjected to three high-stringency washes in 0.1 X SSC at 52°C for 20 minutes each. Following the series of washes, cryosections were dehydrated by consecutive exposure to 70%, 95%, and 100% ammonium acetate in alcohol, followed by air drying and exposure to Kodak
15 BioMax MR-1 film. After 13 days of exposure, the film was developed. Based on these results, brain sections that gave rise to positive hybridization signals were coated with Kodak NTB-2 nuclear track emulsion and the slides were stored in the dark for 32 days. The slides were then developed and counterstained with hematoxylin. Emulsion-coated sections were analyzed microscopically to determine the specificity
20 of labeling. The signal was determined to be specific if autoradiographic grains (generated by antisense probe hybridization) were clearly associated with crystal violet-stained cell bodies. Autoradiographic grains found between cell bodies indicates non-specific binding.

Specific labeling with the antisense probe occurred at low levels in the
25 cortex and in the substantia nigra-pars compacta (SN-c). The specificity of labeling was confirmed by microscopic analysis of emulsion-coated cryosections, as described above. In contrast, hybridization using the riboprobe specific for the sense strand of CON193 did not result in specific tissue labeling. The observed regional distribution of CON193 mRNA suggests that ligands for this GPCR may be involved in signal
30 transductions important for cellular processes underlying neurological functioning. In addition, expression of CON193 in the brain provides an indication that modulators of

- 101 -

CON193 activity have utility for treating neurological disorders, including but not limited to, schizophrenia, depression, anxiety, bipolar disease, epilepsy, neuritis, neurasthenia, neuropathy, neuroses, and the like. Use of CON193 modulators, including CON193 ligands and anti-CON193 antibodies, to treat individuals having such disease states is intended as an aspect of the invention.

B. CON166

A CON166-specific probe was generated using PCR as described above for CON193 in Example 3A (but using CON166-specific primers). The probe consisted of a 259 bp fragment containing sequence at the 3' end of CON-166 (nucleotides 715-974 of SEQ ID NO:1) and containing terminal *EcoRI* and *BamHI* restriction sites. The riboprobes were labeled with [³⁵S]-UTP to yield a specific activity of 0.40×10^6 cpm/pmol for antisense riboprobes and 0.65×10^6 cpm/pmol for sense-strand riboprobes. Hybridization with the riboprobes and subsequent washing of the slides was carried out as described above for CON193 in Example 3A.

Specific labeling with the antisense probe occurred in cortical regions, including the piriform complex, neostriatum, thalamus and hippocampus. The specificity of labeling was confirmed by microscopic analysis of emulsion-coated cryosections. These sections revealed that the autoradiographic grains resulting from antisense riboprobe *in situ* hybridizations were distributed over cell bodies rather than trapped between cell bodies. In contrast, hybridization using the riboprobe specific for the sense strand of CON166 produced a faint signal in the hippocampus only, but even this signal was found to be non-specific upon microscopic examination. The observed regional distribution of CON166 mRNA suggests that ligands for this GPCR may be involved in signal transductions important for cellular processes underlying neurological functioning. In addition, expression of CON166 in the brain provides an indication that modulators of CON166 activity have utility for treating neurological disorders, including but not limited to, schizophrenia, affective disorders, ADHD/ADD (*i.e.*, Attention Deficit-Hyperactivity Disorder/Attention Deficit Disorder), and neural disorders such as Alzheimer's disease, Parkinson's disease, migraine, and senile dementia. Some other diseases for which modulators of

- 102 -

CON166 may have utility include depression, anxiety, bipolar disease, epilepsy, neuritis, neurasthenia, neuropathy, neuroses, and the like. Use of CON166 modulators, including CON166 ligands and anti-CON166 antibodies, to treat individuals having such disease states is intended as an aspect of the invention.

5

C. CON 103

A cocktail of two CON103-specific antisense oligonucleotide probes (CON103a and CON103b) were used because of the relatively high GC content of the CON103 coding region. The CON103a sequence
10 (5'TTTATTAATATTGGAAGGGACAAACTGGAGAGCACAGAACAT3'; SEQ ID NO: 72) corresponds to the reverse complement of nucleotides 2196-2237 of SEQ ID NO: 5 and CON103b sequence (5'AAAGCCACCATGGA
AGCCATGCCAAAGATGATGCTGGGCAAGAA 3'; SEQ ID NO: 73) corresponds to the reverse complement of nucleotides 195-1538 of SEQ ID NO: 5. Terminal
15 deoxynucleotidyltransferase and [α -³³P]dATP were used to 3' end-label CON103a (1.36 x 10⁷ cpm/pmol) and CON103b (9.1 x 10⁶ cpm/pmol). The probes were denatured by incubation at 70°C for three minutes and added to hybridization buffer containing 50% formamide, 10% dextran, 0.3 M NaCl, 10 mM Tris (pH 8.0), 1 mM EDTA, 1X Denhardt's Solution, and 200 mM dithiothreitol. The final concentration
20 of each radiolabeled probe was 2 pmol/ml of hybridization solution. Microscope slides containing sequential brain cryosections were independently exposed to 45 μ l of hybridization solution (containing the antisense oligonucleotide probes CON103a and CON103b) per slide and silanized cover slips were placed over the sections being exposed to hybridization solution. Sections were incubated overnight (15-18 hours) at
25 37°C to allow hybridization to occur.

Following the hybridization period, coverslips were washed off the slides in 1X SSC. The cryosections were then subjected to three high-stringency washes in 1 X SSC at 65°C for 20 minutes each. Following two room-temperature washes, cryosections were dehydrated by consecutive exposure to 70%, 95%, and
30 100% ethanol (0.3 M ammonium acetate added to 70% and 95% ethanol solutions), followed by air drying and exposure to Kodak BioMax MR-1 film. After 28 days of

- 103 -

exposure, the film was developed. Based on these results, brain sections that showed positive hybridization signals were coated with Kodak NTB-2 nuclear track emulsion and the slides were stored in the dark for four months. The slides were then developed and counterstained with hematoxylin. Emulsion-coated sections were analyzed microscopically to determine the specificity of labeling. The signal was determined to be specific if autoradiographic grains (generated by antisense probe hybridization) were present over cell bodies and not trapped between cell bodies.

Specific labeling with the antisense probe occurred in all cortical regions, including the piriform cortex and hippocampus. The specificity of labeling was confirmed by microscopic analysis of emulsion-coated cryosections. These sections revealed that the autoradiographic grains resulting from antisense riboprobe *in situ* hybridizations were distributed over cell bodies rather than trapped between cell bodies. The observed distribution of CON103 mRNA in the cortical and paralimbic regions of the mammalian brain suggests that ligands for this GPCR may be involved in signal transductions important for cellular processes underlying neurological functioning. In addition, expression of CON103 in the brain provides an indication that modulators of CON103 activity have utility for treating neurological and neuropsychiatric disorders, including but not limited to, schizophrenia, depression, anxiety, attention deficit disorder (with or without hyperactivity), bipolar disease, epilepsy, migraine, neuritis, neurasthenia, neuropathy, neuroses, obesity, Parkinson's disease, other dementias, and the like. Use of CON103 modulators, including CON103 ligands and anti-CON103 antibodies, to treat individuals having such disease states is intended as an aspect of the invention.

D. CON203

CON203-specific cRNA probes were prepared using conventional techniques. Initially, a 293 bp fragment of the CON203 coding region, with a *Bam*HI site and an *Eco*RI site disposed on opposite ends, was prepared by PCR using primers LW1314 (5'-GCATGAATTCCCACCTTCATCATCTACCTC-3'; SEQ ID NO: 40) and LW1315 (5'-GCATGGATCCGAAGACCAAAAAGACCCAG-3'; SEQ ID NO: 41). LW1314 includes an *Eco*RI site and additional protective residues at its 5'

terminus, with the rest of the sequence corresponding to CON203 coding nucleotides 164-183, which correspond to positions 309-328 of SEQ ID NO: 7. LW1315 includes 5' protective nucleotides and a *Bam*HI site, with the rest of the sequence corresponding to the complement of CON203 coding nucleotides 438-456, which
5 correspond to positions 583-601 of SEQ ID NO: 7. The PCR-amplified fragment was then digested with *Bam*HI and *Eco*RI and ligated into the corresponding sites of pBluescript II to yield pCon203 BS. The recombinant clone was then linearized either with *Bam*HI or *Eco*RI. Linearization with *Bam*HI provided a substrate for *in vitro* expression of a sense-strand cRNA probe using the vector-borne T7 promoter.
10 Digestion with *Eco*RI was used to provide a substrate for *in vitro* transcription using the vector-borne T3 promoter to generate an anti-sense cRNA probe. *In vitro* transcriptions were performed in the presence of [³⁵S] UTP, thereby yielding sense- and anti-sense strand riboprobes having specific radioactivities of 5.38×10^7 cpm/pmol and 5.34×10^7 cpm/pmol, respectively. Hybridization with the riboprobes
15 and subsequent washing of the slides was carried out as described above for CON193 in Example 3A. Subsequently, the slides were exposed to Kodak BioMax MR-1 film. After 9 days of exposure, the film was developed. Based on these results, brain sections that gave rise to positive hybridization signals were coated with Kodak NTB-2 nuclear track emulsion and the slides were stored in the dark for 25 days. The
20 slides were then developed as described above for CON193 in Example 3A.

Specific labeling with the antisense probe occurred in several limbic and paralimbic regions, as well as areas thought to be involved in voluntary motor control. In particular, the probe hybridized to CON203 mRNAs in the following regions of the brain: cortical regions, including the piriform cortex, neostriatum,
25 lateral olfactory tract, hypothalamic nuclei, bed nucleus of the stria terminalis, amygdala, hippocampus, reticular thalamus and other thalamic regions, subthalamic nucleus, and the red nucleus. The specificity of labeling was confirmed by microscopic analysis of emulsion-coated cryosections. These sections revealed that the autoradiographic grains resulting from antisense riboprobe *in situ* hybridizations
30 were distributed over cell bodies rather than trapped between cell bodies. Confirming expression of CON203 mRNA, the sense-strand riboprobe did not show specific

- 105 -

hybridization. The observed distribution of CON203 mRNA in the cortical (particularly, motor circuits) and paralimbic regions of the mammalian brain suggests that CON203 and the ligands for this GPCR may be involved in signal transductions important for cellular processes underlying neurological functioning. In addition, expression of CON203 in the brain provides an indication that modulators of CON203 activity have utility for treating neurological disorders, including but not limited to, schizophrenia, depression, anxiety, bipolar disease, epilepsy, migraine, attention deficit disorder (with or without hyperactivity), neuritis, neurasthenia, neuropathy, neuroses, Parkinson's disease, dementia, obesity, and the like. Use of CON203 modulators, including CON203 ligands and anti-CON203 antibodies, to treat individuals having such disease states is intended as an aspect of the invention.

E. CON198

A 266 bp fragment of CON198 containing *Eco*RI and *Bam*HI restriction sites was amplified from the full-length clone by PCR, using the primers LW1308: 5'-GCATGAATTCACTCACTTCTCATCTCCTTC-3' (SEQ ID NO: 46) and LW1309: 5'-GCATGGATCCAATCTCCTTTGTCTTCACTC-3' (SEQ ID NO: 47) Primer LW1308 contains an *Eco*RI site (underlined) followed by sequence identical to nucleotides 638-657 of SEQ ID NO: 9. Primer LW1309 contain a *Bam*HI site (underlined) followed by sequence complementary to nucleotides 903-884 of SEQ ID NO: 9. The amplification product was digested with *Eco*RI and *Bam*HI, and then subcloned into an *Eco*RI- and *Bam*HI-digested pBluescript II vector (*Stratagene*). The 266 amplified and subcloned basepairs correspond to nucleotides 638 to 903 of SEQ ID NO: 9.

The subcloned CON198-Bluescript construct was used to generate strand-specific probes for the *in situ* hybridization experiments. The construct was linearized with *Bam*HI, for labeling with T7 polymerase (sense), or *Eco*RI, for T3 polymerase (antisense), and used as a template for *in vitro* transcription of sense and antisense cRNA riboprobes. The riboprobes were labeled with ³⁵S-UTP to yield a specific activity of 0.45 x 10⁶ cpm/pmol for antisense and 0.732 x 10⁶ cpm/pmol for

- 106 -

sense probe. Hybridization with the riboprobes and subsequent washing of the slides was carried out as described above for CON193 in Example 3A.

Specific labeling with the antisense probe showed distribution of CON198 mRNA in the rat brain in several limbic and paralimbic regions as well as areas thought to be involved in voluntary motor control. Labelled regions included cortical regions, piriform cortex, hypothalamic nuclei (paraventricular nucleus, supraoptic nucleus, suprachiasmatic nucleus), hippocampus, reticular thalamus, substantia nigra-pars compacta (SN-C), ventral tegmental area, and the red nucleus. The specificity of labeling was confirmed by microscopic analysis of emulsion coated sections. These sections revealed that the autoradiographic grains generated by the antisense probe were distributed over cell bodies rather than trapped between cell bodies. Sense probe did not generate specific labeling.

The observed regional distribution of CON198 mRNA provides a therapeutic indication for natural ligands for CON198 as well as modulators of CON198 activity, such as anti-CON198 antibody substances or small molecules that agonize or antagonize ligand-mediated CON198 signalling. In particular, the expression pattern provides an indication that such molecules will have utility for treating neurological and/or psychiatric diseases, including but not limited to schizophrenia, depression, anxiety, bipolar disease, affective disorders, ADHD/ADD, epilepsy, neuritis, neurasthenia, neuropathy, neuroses, Alzheimer's disease, Parkinson's disease, migraine, senile dementia, and the like. Use of CON198 modulators, including CON198 ligands and anti-CON198 antibodies, to treat individuals having such disease states is intended as an aspect of the invention. Such modulators are administered by any means effective to safely deliver the modulators to the CON198-expressing cells, including but not limited to oral administration, inhalation, or injection of compositions comprising the modulators in a pharmaceutically acceptable diluent, adjuvant, or carrier. Efficacy of treatment can initially be determined in any accepted animal model that provides a biochemical or behavioral marker that correlates with disease severity or treatment efficacy.

F. CON197

A 261 bp fragment of CON197 containing *EcoRI* and *BamHI* restriction sites was amplified from the full-length clone by PCR, using the primers LW1306: 5'-GCATGAATTCTTCTACTTCATCATCCTCC-3' (SEQ ID NO: 50) and
5 LW1307: 5'-GCATGGATCCAAAGGCCATCACAACAAG-3' (SEQ ID NO: 51).
Primer LW1306 includes sequence identical to nucleotides 100-118 of SEQ ID NO: 11 (underlined), preceded by an *EcoRI* site. Primer LW1307 includes sequence complementary to nucleotides 361-343 of SEQ ID NO: 11 (underlined), preceded by a *BamHI* restriction site. The amplification product was digested with *EcoRI* and
10 *BamHI*, and then subcloned into an *EcoRI*- and *BamHI*-digested pBluescript II vector (Stratagene). The 261 amplified and subcloned basepairs correspond to nucleotides 100 to 361 of SEQ ID NO: 11.

The subcloned CON197-Bluescript construct was used to generate strand-specific probes for the *in situ* hybridization experiments. The construct was
15 linearized with *BamHI*, for labeling with T7 polymerase (sense), or *EcoRI*, for T3 polymerase (antisense), and used as a template for *in vitro* transcription of sense and antisense cRNA riboprobes. The riboprobes were labeled with ³⁵S-UTP to yield a specific activity of 0.51 x 10⁶ cpm/pmol for antisense and 0.432 x 10⁶ cpm/pmol for sense probe. Hybridization with the riboprobes and subsequent washing of the slides
20 was carried out as described above for CON193 in Example 3A.

Specific labeling with the antisense probe showed wide spread distribution of CON197 mRNA in the rat brain. Labelled regions included neo and allo cortex, piriform cortex, neostriatum, thalamic nuclei, hypothalamic nuclei, hippocampus, amygdala, cerebellum, and the olfactory bulb. The specificity of
25 labeling was confirmed by microscopic analysis of emulsion coated sections. These sections revealed that the autoradiographic grains generated by the antisense probe were distributed over cell bodies rather than trapped between cell bodies. Sense probe did not generate specific labeling.

The observed regional distribution of CON197 mRNA provides a
30 therapeutic indication for natural ligands for CON197 as well as modulators of CON197 activity, such as anti-CON197 antibody substances or small molecules that

- 108 -

agonize or antagonize ligand-mediated CON197 signalling. In particular, the expression pattern provides an indication that such molecules will have utility for treating neurological and/or psychiatric diseases, including but not limited to dementia, schizophrenia, depression, anxiety, bipolar disease, migraine, Parkinson's disease, affective disorders, Alzheimer's disease, senile dementia, attention deficit hyperactivity disorder/attention deficit disorder (ADHD/ADD), epilepsy, neuritis, neurasthenia, neuropathy, neuroses, and the like. Use of CON197 modulators, including CON197 ligands and anti-CON197 antibodies, to treat individuals having such disease states is intended as an aspect of the invention. Such modulators are administered by any means effective to safely deliver the modulators to the CON197-expressing cells, including but not limited to oral administration, inhalation, or injection of compositions comprising the modulators in a pharmaceutically acceptable diluent, adjuvant, or carrier. Efficacy of treatment can initially be determined in any accepted animal model that provides a biochemical or behavioral marker that correlates with disease severity or treatment efficacy.

G. CON202

A 272 bp fragment of CON202 containing EcoRI and BamHI restriction sites was amplified from the full-length clone by PCR, using the primers LW1310 GCATGAATTCGCAGAAGAAGGCTATTGG (SEQ ID NO: 56) and LW1311 GCATGGATCCGCAGTAAAGAAGGGTTGTG (SEQ ID NO: 57). The amplification product was digested with EcoRI and BamHI, and then subcloned into a pBluescript II vector (Stratagene) that was digested with EcoRI and BamHI. The 272 amplified and subcloned basepairs correspond to nucleotides 1065 to 1336 of SEQ ID NO: 13.

The subcloned CON202-Bluescript construct was used to generate strand-specific probes for the *in situ* hybridization experiments. The construct was linearized with BamHI, for labeling with T7 polymerase (sense), or EcoRI, for T3 polymerase (antisense), and used as a template for *in vitro* transcription of sense and antisense cRNA riboprobes. The riboprobes were labeled with ^{35}S -UTP to yield a specific activity of 4.7×10^5 cpm/pmol for antisense and 4.3×10^5 cpm/pmol for sense

- 109 -

probe. Hybridization with the riboprobes and subsequent washing of the slides was carried out as described above for CON193 in Example 3A.

Specific labeling with the antisense probe showed wide spread distribution of CON202 mRNA in the rat brain. Labelled regions included the cortical regions, lateral olfactory nuclei, hippocampus, subthalamic nucleus, and at a lower level, the nigra-pars compacta.

The observed regional distribution of CON202 mRNA provides a therapeutic indication for natural ligands for CON202 as well as modulators of CON202 activity, such as anti-CON202 antibody substances or small molecules that agonize or antagonize ligand-mediated CON202 signaling. In particular, the expression pattern provides an indication that such molecules will have utility for treating neurological and/or psychiatric diseases, including but not limited to schizophrenia, affective disorders, attention deficit hyperactivity disorder/attention deficit disorder, depression, anxiety, bipolar disease, epilepsy, neuritis, neurasthenia, neuropathy, neuroses, Alzheimer's disease, Parkinson's disease, migraine, senile dementia and the like. Use of CON202 modulators, including CON202 ligands and anti-CON202 antibodies, to treat individuals having such disease states is intended as an aspect of the invention. Such modulators are administered by any means effective to safely deliver the modulators to the CON202-expressing cells, including but not limited to oral administration, inhalation, or injection of compositions comprising the modulators in a pharmaceutically acceptable diluent, adjuvant, or carrier. Efficacy of treatment can initially be determined in any accepted animal model that provides a biochemical or behavioral marker that correlates with disease severity or treatment efficacy.

H. CON222

A 264 bp fragment of CON222 containing EcoRI and BamHI restriction sites was amplified from the full-length clone by PCR, using the primers LW1472 (5'GCATGAATTCTGCCATGTCAATCATTTCTCTC3'; SEQ ID NO: 62, EcoRI site is underlined) and LW1473 (5'GCATGGATCCGTTCTGCATTTTCC-AGGTCTC3'; SEQ ID NO: 63, BamHI site is underlined). The amplification product

- 110 -

was digested with EcoRI and BamHI, and then subcloned into a predigested pBluescript II vector (Stratagene). The 264 amplified and subcloned basepairs correspond to nucleotides 237 to 500 of SEQ ID NO: 15.

5 The subcloned CON222-Bluescript construct was used to generate strand-specific probes for the *in situ* hybridization experiments. The construct was linearized with BamHI, for labeling with T7 polymerase (sense), or EcoRI, for T3 polymerase (antisense), and used as a template for *in vitro* transcription of sense and antisense cRNA riboprobes. The riboprobes were labeled with ³⁵S-UTP to yield a specific activity of 4.25×10^5 cpm/pmol for antisense and 3.9×10^5 cpm/pmol for
10 sense probe. Hybridization with the riboprobes and subsequent washing of the slides was carried out as described above for CON193 in Example 3A.

Specific labeling with the antisense probe showed wide spread distribution of CON222 mRNA in the rat brain. Labelled regions included the cortical regions, piriform cortex, striatum, hippocampus, thalamus, hypothalamus,
15 dorsal raphe, and habenula.

The observed regional distribution of CON222 mRNA provides a therapeutic indication for natural ligands for CON222 as well as modulators of CON222 activity, such as anti-CON222 antibody substances or small molecules that agonize or antagonize ligand-mediated CON222 signaling. In particular, the
20 expression pattern provides an indication that such molecules will have utility for treating neurological and/or psychiatric diseases, including but not limited to schizophrenia, affective disorders, attention deficit hyperactivity disorder/attention deficit disorder, depression, anxiety, bipolar disease, epilepsy, neuritis, neurasthenia, neuropathy, neuroses, Alzheimer's disease, Parkinson's Disease, migraine, senile
25 dementia, and the like. Use of CON222 modulators, including CON222 ligands and anti-CON222 antibodies, to treat individuals having such disease states is intended as an aspect of the invention. Such modulators are administered by any means effective to safely deliver the modulators to the CON222-expressing cells, including but not limited to oral administration, inhalation, or injection of compositions comprising the
30 modulators in a pharmaceutically acceptable diluent, adjuvant, or carrier. Efficacy of treatment can initially be determined in any accepted animal model that provides a

- 111 -

biochemical or behavioral marker that correlates with disease severity or treatment efficacy.

I. CON215

5 A 261 bp fragment of CON215 containing *EcoRI* and *BamHI* restriction sites was amplified from the full-length clone by PCR, using the primers LW1411: 5'-GCATGAATTCTGCCAAACATCATCCTGAC-3' (SEQ ID NO: 64) and LW1412: 5'-GCATGGATCCTACACAGCCACAACAACCC-3' (SEQ ID NO: 65). Primer LW1411 contains an *EcoRI* site (underlined) followed by sequence 10 identical to CON215 coding nucleotides 521-537, which correspond to positions 533-549 of SEQ ID NO: 17. Primer LW1412 contain a *BamHI* site (underlined) followed by sequence complementary to CON215 coding nucleotides 764-781, which correspond to positions 776-793 of SEQ ID NO: 17. The amplification product was digested with *EcoRI* and *BamHI*, and then subcloned into an *EcoRI*- and *BamHI*- 15 digested pBluescript II vector (*Stratagene*). The 261 amplified and subcloned basepairs correspond to nucleotides 521 to 781 of SEQ ID NO: 17.

The subcloned CON215-Bluescript construct was used to generate strand-specific probes for the *in situ* hybridization experiments. The construct was linearized with *BamHI*, for labeling with T7 polymerase (sense), or *EcoRI*, for T3 20 polymerase (antisense), and used as a template for *in vitro* transcription of sense and antisense cRNA riboprobes. The riboprobes were labeled with ³⁵S-UTP to yield a specific activity of 48.03 x 10⁶ cpm/pmol for antisense and 48.09 x 10⁶ cpm/pmol for sense probe. Hybridization with the riboprobes and subsequent washing of the slides was carried out as described above for CON193 in Example 3A.

25 Subsequently, the slides were exposed to Kodak BioMax MR-1 film. After 9 days of exposure, the film was developed. Slides containing sections that showed a hybridization signal on film autoradiograms were coated with Kodak NTB-2 nuclear track emulsion and stored in the dark for 25 days. The slides were then developed as described above for CON193 in Example 3A.

30 Specific labeling with the antisense probe showed distribution of CON215 mRNA in the rat brain in limbic endocrine and motor circuits. Specifically,

- 112 -

CON215 mRNA was present in the cortex, hippocampus, and red nucleus. The specificity of labeling was confirmed by microscopic analysis of emulsion coated sections. These sections revealed that the autoradiographic grains generated by the antisense probe were distributed over cell bodies rather than trapped between cell
5 bodies. Sense probe did not generate specific labeling.

The observed regional distribution of CON215 mRNA provides a therapeutic indication for natural ligands for CON215 as well as modulators of CON215 activity, such as anti-CON215 antibody substances or small molecules that agonize or antagonize ligand-mediated CON215 signaling. In particular, the
10 expression pattern provides an indication that such molecules will have utility for treating neurological and/or psychiatric diseases, including but not limited to schizophrenia, depression, anxiety, bipolar disease, epilepsy, migraine, attention deficit (with or without hyperactive disorder), neuritis, neuasthenia, neuropathy, neuroses, Parkinson's disease, dementia, obesity, and the like. Use of CON215
15 modulators, including CON215 ligands and anti-CON215 antibodies, to treat individuals having such disease states is intended as an aspect of the invention.

Such modulators are administered by any means effective to safely deliver the modulators to the CON215-expressing cells, including but not limited to oral administration, inhalation, or injection of compositions comprising the
20 modulators in a pharmaceutically acceptable diluent, adjuvant, or carrier. Efficacy of treatment can initially be determined in any accepted animal model that provides a biochemical or behavioral marker that correlates with disease severity or treatment efficacy.

25 J. CON 217

Two oligonucleotides were designed based on SEQ ID NO: 19 and obtained from Sigma-Genosys (St. Louis, MO) to use as probes for *in situ* hybridization. The first oligonucleotide, designated 217A, has the sequence
5'TAGGTCGGTAGTCAGGACACGGGAGAACAGAACTGTTGGTTGA3' (SEQ
30 ID NO: 68) which is complementary to nucleotides 102 to 60 of SEQ ID NO: 19. The second oligonucleotide, designated 217B, has the sequence

- 113 -

5'GCCCCTGTGGCGGTTTAGATCCAGAATGCCCATTTTCTGTTCCATCTAAC
CA3' (SEQ ID NO: 69) which corresponds to the complement of nucleotides 1530 to
1479 of SEQ ID NO: 17. Both oligonucleotides, 217A and 217B, were reconstituted
with 1x TE buffer to a concentration of 20 pMol/ml and labeled with ³³P-dATP to
yield a specific activity of 2.08 x 10⁶ and 1.53 x 10⁶ cpm/ml, respectively.

Hybridization was carried out at 37°C overnight as described above for
CON193 in Example 3A. Following the hybridizations, the coverslips were washed
off the slides with 1x SSC for 45 minutes. The slides were then washed for 20
minutes at room temperature in 1x SSC followed by three high stringency washes in
1x SSC at 65°C. After washing, the slides were dehydrated with 70%, 95%, and
100% ethanol containing 0.3 mM NH₄OAc, air-dried, and exposed to Kodak BioMax
MR-1 film. After 21 days of exposure, the film was developed. Based on these
results, sections that showed a hybridization signal on film autoradiography were
coated with Kodak NTB-2 nuclear track emulsion and stored in the dark for 42 days.
The slides were then developed and counterstained with hematoxylin. Emulsion-
coated sections were analyzed microscopically to determine the specificity of labeling.
The signal was judged to be specific if autoradiographic grains (generated by
antisense probe hybridization) were associated clearly with crystal violet stained cell
bodies. Autoradiographic grains found between cell bodies were deemed non-
specific.

Specific labeling with the antisense probe showed wide spread
distribution of CON217 mRNA in the rat brain. Labelled regions included the cortex,
piriform cortex, hippocampus, cerebellum, medulla, spinal cord, temporal lobe,
putamen, substantia nigra and thalamus.

The observed regional distribution of CON217 mRNAs provide a
therapeutic indication for natural ligands for these G protein-coupled receptors as well
as modulators of their activity, such as anti-CON217 antibody substances or small
molecules that mimic, agonize or antagonize ligand-mediated CON217 signaling. In
particular, the expression patterns provide an indication that such molecules will have
utility for treating neurological and/or psychiatric diseases, including but not limited
to schizophrenia, affective disorders, attention deficit hyperactivity disorder/attention

- 114 -

deficit disorder, depression, anxiety, bipolar disease, epilepsy, neuritis, neurasthenia, neuropathy, neuroses, Alzheimer's disease, Parkinson's Disease, migraine, senile dementia, and the like. Use of CON217 polypeptide modulators, including CON217 ligands and anti-CON217 polypeptide antibodies, to treat individuals having such

5 disease states is intended as an aspect of the invention. Such modulators are administered by any means effective to safely deliver the modulators to the GPCR polypeptide-expressing cells, including but not limited to oral administration, inhalation, or injection of compositions comprising the modulators in a pharmaceutically acceptable diluent, adjuvant, or carrier. Efficacy of treatment can

10 initially be determined in any accepted animal model that provides a biochemical or behavioral marker that correlates with disease severity or treatment efficacy.

EXAMPLE 4

Recombinant Expression of GPCR Polypeptides in Eukaryotic Host Cells

15 To produce GPCR protein, a GPCR polypeptide-encoding polynucleotide is expressed in a suitable host cell using a suitable expression vector, using standard genetic engineering techniques. For example, one of the GPCR polypeptide-encoding sequences described in Example 1 (such as SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17 or 19) is subcloned into the commercial expression vector

20 pzeoSV2 (Invitrogen, San Diego, CA) and transfected into Chinese Hamster Ovary (CHO) cells (ATCC CRL-1781) using the transfection reagent fuGENE 6 (Boehringer-Mannheim) and the transfection protocol provided in the product insert. Additional eukaryotic cell lines, such as African Green Monkey Kidney cells (COS-7, ATCC CRL-1651) or Human Kidney cells (HEK 293, ATCC CRL-1573), may be

25 used as well. Cells stably expressing a GPCR polypeptide (e.g., CON193, CON166, CON103, CON203, CON198, CON197, CON202, CON222, CON215, or CON217) are selected by growth in the presence of 100 mg/ml zeocin (Stratagene, LaJolla, CA). Optionally, GPCR polypeptide is purified from the cells using standard chromatographic techniques. To facilitate purification, antisera is raised against one

30 or more synthetic peptide sequences that correspond to portions of the GPCR amino acid sequence, and the antisera is used to affinity purify GPCR polypeptides. The

- 115 -

GPCR gene also may be expressed in frame with a tag sequence (e.g., polyhistidine, hemagglutinin, FLAG) to facilitate purification. Moreover, it will be appreciated that many of the uses for GPCR polypeptides, such as assays described below, do not require purification of GPCR polypeptides from the host cell.

5

EXAMPLE 5

Antibodies to GPCR Polypeptides

Standard techniques are employed to generate polyclonal or monoclonal antibodies to the GPCR receptors (e.g., CON193, CON166, CON103, 10 CON203, CON198, CON197, CON202, CON222, CON215, or CON217), and to generate useful antigen-binding fragments thereof or variants thereof, including "humanized" variants. Such protocols can be found, for example, in Sambrook *et al.*, *Molecular Cloning: a Laboratory Manual*. Second Edition, Cold Spring Harbor, New York: Cold Spring Harbor Laboratory (1989); Harlow *et al.* (Eds), *Antibodies A* 15 *Laboratory Manual*; Cold Spring Harbor Laboratory; Cold Spring Harbor, NY (1988); and other documents cited below. In one embodiment, recombinant GPCR polypeptides (or cells or cell membranes containing such polypeptides) of the invention are used as an antigen to generate the antibodies. In another embodiment, one or more peptides having amino acid sequences corresponding to an immunogenic 20 portion of a GPCR polypeptide (e.g., 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, or more amino acids) are used as antigen. Peptides corresponding to extracellular portions of GPCR polypeptides, especially hydrophilic extracellular portions, are preferred. The antigen may be mixed with an adjuvant or linked to a hapten to increase antibody production.

25

A. Polyclonal or Monoclonal antibodies

As one exemplary protocol, a recombinant GPCR polypeptide or synthetic fragment thereof is used to immunize a mouse for generation of monoclonal antibodies (or larger mammal, such as a rabbit, for polyclonal antibodies). To 30 increase antigenicity, peptides are conjugated to Keyhole Limpet Hemocyanine (Pierce), according to the manufacturer's recommendations. For an initial injection,

- 116 -

the antigen is emulsified with Freund's Complete Adjuvant and injected subcutaneously. At intervals of two to three weeks, additional aliquots of GPCR antigen are emulsified with Freund's Incomplete Adjuvant and injected subcutaneously. Prior to the final booster injection, a serum sample is taken from the immunized mice and assayed by Western blot to confirm the presence of antibodies that immunoreact with GPCR polypeptide. Serum from the immunized animals may be used as a polyclonal antiserum or used to isolate polyclonal antibodies that recognize GPCR polypeptide. Alternatively, the mice are sacrificed and their spleen removed for generation of monoclonal antibodies.

To generate monoclonal antibodies, the spleens are placed in 10 ml serum-free RPMI 1640, and single cell suspensions are formed by grinding the spleens in serum-free RPMI 1640, supplemented with 2 mM L-glutamine, 1 mM sodium pyruvate, 100 units/ml penicillin, and 100 µg/ml streptomycin (RPMI) (Gibco, Canada). The cell suspensions are filtered and washed by centrifugation and resuspended in serum-free RPMI. Thymocytes taken from three naive Balb/c mice are prepared in a similar manner and used as a Feeder Layer. NS-1 myeloma cells, kept in log phase in RPMI with 10% fetal bovine serum (FBS) (Hyclone Laboratories, Inc., Logan, Utah) for three days prior to fusion, are centrifuged and washed as well.

To produce hybridoma fusions, spleen cells from the immunized mice are combined with NS-1 cells and centrifuged, and the supernatant is aspirated. The cell pellet is dislodged by tapping the tube, and 2 ml of 37°C PEG 1500 (50% in 75mM Hepes, pH 8.0) (Boehringer Mannheim) is stirred into the pellet, followed by the addition of serum-free RPMI. Thereafter, the cells are centrifuged and resuspended in RPMI containing 15% FBS, 100 µM sodium hypoxanthine, 0.4 µM aminopterin, 16 µM thymidine (HAT) (Gibco), 25 units/ml of IL-6 (Boehringer Mannheim) and 1.5×10^6 thymocytes/ml and plated into 10 Corning flat-bottom 96-well tissue culture plates (Corning, Corning New York).

On days 2, 4, and 6, after the fusion, 100 µl of medium is removed from the wells of the fusion plates and replaced with fresh medium. On day 8, the fusions are screened by ELISA, testing for the presence of mouse IgG that binds to a

- 117 -

GPCR polypeptide. Selected fusion wells are further cloned by dilution until monoclonal cultures producing anti-GPCR polypeptide antibodies are obtained.

B. Humanization of Anti-GPCR Monoclonal Antibodies

5 The expression patterns of GPCR polypeptides as reported herein and the proven track record of GPCR's as targets for therapeutic intervention suggest therapeutic indications for GPCR polypeptide inhibitors (antagonists). GPCR polypeptide-neutralizing antibodies comprise one class of therapeutics useful as antagonists. Following are protocols to improve the utility of anti-GPCR polypeptide monoclonal antibodies as therapeutics in humans, by "humanizing" the monoclonal antibodies to improve their serum half-life and render them less immunogenic in human hosts (*i.e.*, to prevent human antibody response to non-human anti-GPCR polypeptide antibodies).

10 The principles of humanization have been described in the literature and are facilitated by the modular arrangement of antibody proteins. To minimize the possibility of binding complement, a humanized antibody of the IgG4 isotype is preferred.

15 For example, a level of humanization is achieved by generating chimeric antibodies comprising the variable domains of non-human antibody proteins of interest with the constant domains of human antibody molecules. (See, *e.g.*, Morrison and Oi, *Adv. Immunol.*, 44:65-92 (1989). The variable domains of GPCR-neutralizing anti-GPCR antibodies are cloned from the genomic DNA of a B-cell hybridoma or from cDNA generated from mRNA isolated from the hybridoma of interest. The V region gene fragments are linked to exons encoding human antibody constant domains, and the resultant construct is expressed in suitable mammalian host cells (*e.g.*, myeloma or CHO cells).

20 To achieve an even greater level of humanization, only those portions of the variable region gene fragments that encode antigen-binding complementarity determining regions ("CDR") of the non-human monoclonal antibody genes are cloned into human antibody sequences. [See, *e.g.*, Jones *et al.*, *Nature*, 321:522-525 (1986); Riechmann *et al.*, *Nature*, 332:323-327 (1988); Verhoeyen *et al.*, *Science*,

- 118 -

239:1534-36 (1988); and Tempest *et al.*, *Bio/Technology*, 9:266-71 (1991). If necessary, the β -sheet framework of the human antibody surrounding the CDR3 regions also is modified to more closely mirror the three dimensional structure of the antigen-binding domain of the original monoclonal antibody. (See Kettleborough
5 *et al.*, *Protein Engin.*, 4:773-783 (1991); and Foote *et al.*, *J. Mol. Biol.*, 224:487-499 (1992).

In an alternative approach, the surface of a non-human monoclonal antibody of interest is humanized by altering selected surface residues of the non-human antibody, *e.g.*, by site-directed mutagenesis, while retaining all of the
10 interior and contacting residues of the non-human antibody. See Padlan, *Molecular Immunol.*, 28(4/5):489-98 (1991).

The foregoing approaches are employed using GPCR-neutralizing anti-GPCR monoclonal antibodies and the hybridomas that produce them to generate humanized GPCR-neutralizing antibodies useful as therapeutics to treat or palliate
15 conditions wherein GPCR expression or ligand-mediated GPCR signaling is detrimental.

C. Human GPCR-Neutralizing Antibodies from Phage Display

Human GPCR-neutralizing antibodies are generated by phage display
20 techniques such as those described in Aujame *et al.*, *Human Antibodies*, 8(4):155-168 (1997); Hoogenboom, *TIBTECH*, 15:62-70 (1997); and Rader *et al.*, *Curr. Opin. Biotechnol.*, 8:503-508 (1997), all of which are incorporated by reference. For example, antibody variable regions in the form of Fab fragments or linked single chain Fv fragments are fused to the amino terminus of filamentous phage minor coat
25 protein pIII. Expression of the fusion protein and incorporation thereof into the mature phage coat results in phage particles that present an antibody on their surface and contain the genetic material encoding the antibody. A phage library comprising such constructs is expressed in bacteria, and the library is panned (screened) for GPCR-specific phage-antibodies using labelled or immobilized GPCR polypeptide as
30 antigen-probe.

- 119 -

D. Human GPCR-Neutralizing Antibodies from Transgenic Mice

Human GPCR-neutralizing antibodies are generated in transgenic mice essentially as described in Bruggemann and Neuberger, *Immunol. Today*, 17(8):391-97 (1996) and Bruggemann and Taussig, *Curr. Opin. Biotechnol.*, 8:455-58 (1997). Transgenic mice carrying human V-gene segments in germline configuration and that express these transgenes in their lymphoid tissue are immunized with a GPCR composition using conventional immunization protocols. Hybridomas are generated using B cells from the immunized mice using conventional protocols and screened to identify hybridomas secreting anti-GPCR human antibodies (*e.g.*, as described above).

EXAMPLE 6**Assays to Identify Modulators of GPCR Polypeptide Activity**

Set forth below are assays for identifying modulators (agonists and antagonists) of GPCR polypeptide activity. Among the modulators that can be identified by these assays include natural ligand compounds of the receptor; synthetic analogs and derivatives of natural ligands; antibodies, antibody fragments, and/or antibody-like compounds derived from natural antibodies or from antibody-like combinatorial libraries; and/or synthetic compounds identified through high throughput screening of libraries; and the like. All modulators that bind GPCR polypeptide are useful for identifying GPCR polypeptide in tissue samples (*e.g.*, for diagnostic purposes, pathological purposes, and the like). Agonist and antagonist modulators are useful for up-regulating and down-regulating GPCR polypeptide activity, respectively, to treat disease states characterized by abnormal levels of GPCR polypeptide activity. GPCR polypeptide binding molecules also may be used to deliver a therapeutic compound or a label to cells that express GPCR polypeptide (*e.g.*, by attaching the compound or label to the binding molecule). The assays may be performed using single putative modulators, and/or may be performed using a known agonist in combination with candidate antagonists (or *visa versa*). Performance of the assays using any of the GPCR polypeptides of the invention described herein (*e.g.*, CON193, CON166, CON103, CON203, CON198, CON197,

- 120 -

CON202, CON222, CON215, or CON217) is contemplated. It will be appreciated that co-transfecting cells with two or more of the receptors for simultaneous screening also is possible.

5 A. cAMP Assays

 In one type of assay, levels of cyclic adenosine monophosphate (cAMP) are measured in GPCR-transfected cells that have been exposed to candidate modulator compounds. Protocols for cAMP assays have been described in the literature. [See, e.g., Sutherland *et al.*, *Circulation*, 37: 279 (1968); Frandsen, E.K. and Krishna, G, *Life Sciences*, 18: 529-541 (1976); Dooley *et al.*, *Journal of Pharmacology and Experimental Therapeutics*, 283 (2): 735-41 (1997); and George *et al.*, *Journal of Biomolecular Screening*, 2 (4): 235-40 (1997).] An exemplary protocol for such an assay, using an Adenylyl Cyclase Activation FlashPlate® Assay from NENTM Life Science Products, is set forth below.

15 Briefly, the GPCR coding sequence (e.g., a cDNA or intronless genomic DNA) is subcloned into a commercial expression vector, such as pzeoSV2 (Invitrogen, San Diego, CA), and transiently transfected into Chinese Hamster Ovary (CHO) cells using known methods, such as the transfection reagent FuGENE 6 (Boehringer-Mannheim) and the transfection protocol provided in the product insert.

20 The transfected CHO cells are seeded into the 96 well microplates from the FlashPlate® assay kit, which are coated with solid scintillant to which antisera to cAMP has been bound. For a control, some wells are seeded with wild type (untransfected) CHO cells. Other wells on the plate receive various amounts of cAMP standard solution for use in creating a standard curve.

25 One or more test compounds are added to the cells in each well, with water and/or compound-free media/diluent serving as a control. After treatment, cAMP is allowed to accumulate in the cells for exactly 15 minutes at room temperature. The assay is terminated by the addition of lysis buffer containing [¹²⁵I]-labelled cAMP, and the plate is counted using a Packard Topcount™ 96-well microplate scintillation counter. Unlabelled cAMP from the lysed cells (or from standards) competes with the fixed amounts of [¹²⁵I]-cAMP for antibody bound to the

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- 121 -

plate. A standard curve is constructed, and cAMP values for the unknowns are obtained by interpolation. Changes in intracellular cAMP level of the cells in response to exposure to a test compound are indicative of GPCR polypeptide modulating activity. Modulators that act as agonists at receptors which couple to the Gs subtype of G-proteins will stimulate production of cAMP, leading to a measurable 3-10 fold increase. Receptor agonists which couple to the Gi/o subtype of G-proteins will inhibit forskolin-stimulated cAMP production, leading to a measurable decrease of 50-100%. Modulators that act as inverse agonists will reverse these effects at receptors that are either constitutively active or activated by known agonists.

B. Aequorin Assays

In another assay cells (e.g., CHO cells) are transiently co-transfected with both a GPCR expression construct and a construct that encodes the photoprotein apoaequorin. In the presence of the cofactor coelenterazine, apoaequorin will emit a measurable luminescence that is proportional to the amount of intracellular (cytoplasmic) free calcium. [See generally Cobbold P.H. and Lee, J.A.C. "Aequorin measurements of cytoplasmic free calcium. In: McCormack J.G. and Cobbold P.H., eds., *Cellular Calcium: A Practical Approach*. Oxford:IRL Press (1991); Stables *et al.*, *Analytical Biochemistry*, 252: 115-26 (1997); and Haugland, R.P. *Handbook of Fluorescent Probes and Research Chemicals*. Sixth edition. Eugene OR: Molecular Probes (1996).]

In one exemplary assay, a GPCR-encoding polynucleotide is subcloned into the commercial expression vector pzeoSV2 (Invitrogen, San Diego, CA) and transiently co-transfected along with a construct that encodes the photoprotein apoaequorin (Molecular Probes, Eugene, OR) into CHO cells using the transfection reagent FuGENE 6 (Boehringer-Mannheim) and the transfection protocol provided in the product insert.

The cells are cultured for 24 hours at 37°C in α MEM (Gibco/BRL, Gaithersburg, MD) supplemented with 10% FBS, 2 mM glutamine, 10 U/ml of penicillin and 10 μ g/ml of streptomycin. Subsequently, the media is changed to serum-free α MEM containing 5 μ M coelenterazine (Molecular Probes, Eugene, OR),

- 122 -

and the cells are cultured for two additional hours at 37°C. Cells are then detached from the plate using VERSEN (Gibco/BRL), washed and resuspended at 2×10^5 cells/ml in serum-free α MEM.

5 Dilutions of candidate GPCR modulator drugs are prepared in serum-free α MEM and dispensed into wells of an opaque 96-well assay plate, 50 μ l/well. Plates are loaded onto an MLX microtiter plate luminometer (Dynex Technologies, Inc., Chantilly, VA). The instrument is programmed to dispense 50 μ l of cell suspension into each well, one well at a time, and immediately read luminescence for 15 seconds. Dose-response curves for the modulator candidates are constructed using
10 the area under the curve for each light signal peak. Data are analyzed with SlideWrite, using the equation for 1-site ligand, and EC_{50} values are obtained. Changes in luminescence caused by the drugs are considered indicative of modulatory activity. Modulators that act as receptor agonists which couple to the Gq subtype of G-proteins give an increase in luminescence of up to 100 fold. Modulators that act as
15 inverse agonists will reverse this effect at receptors that are either constitutively active or activated by known agonists.

C. Luciferase Reporter Gene Assay

The photoprotein luciferase provides another useful tool for assaying
20 for modulators of GPCR activity. Cells (*e.g.*, CHO cells or COS 7 cells) are transiently co-transfected with both a GPCR expression construct (*e.g.*, GPCR-encoding sequence in pzeoSV2 (Invitrogen, San Diego, CA)) and a reporter construct which includes a gene for the luciferase protein downstream from a transcription factor, either cAMP-response element (CRE), AP-1, or NF kappa B. Agonist binding
25 to receptors coupled to the Gs subtype of G-proteins leads to increases in cAMP, activating the CRE transcription factor and resulting in expression of the luciferase gene. Agonist binding to receptors coupled to the Gq subtype of G-protein leads to production of diacylglycerol that activates protein kinase C. As a result, the AP-1 or NF kappa B transcription factors are activated which stimulate expression of the
30 luciferase gene. Expression levels of luciferase reflect the activation status of the signaling events. [See generally George *et al.*, *Journal of Biomolecular Screening*.

2(4): 235-40 (1997); and Stratowa *et al.*, *Current Opinion in Biotechnology*, 6: 574-81 (1995).] Luciferase activity may be quantitatively measured using, *e.g.*, luciferase assay reagents that are commercially available from Promega (Madison, WI).

5 In one exemplary assay, CHO cells are plated in 24-well culture dishes at a density of 100,000 cells/well one day prior to transfection and cultured at 37°C in α MEM (Gibco/BRL, Gaithersburg, MD) supplemented with 10% FBS, 2 mM glutamine, 10 U/ml penicillin and 10 μ g/ml streptomycin. Cells are transiently co-transfected with both a GPCR expression construct and a reporter construct containing the luciferase gene. The reporter plasmids CRE-luciferase, AP-1-luciferase
10 and NF kappa B-luciferase may be purchased from Stratagene (LaJolla, CA). Transfections are performed using FuGENE 6 transfection reagent (Boehringer-Mannheim), and the protocol provided in the product insert. Cells transfected with the reporter construct alone are used as a control. Twenty-four hours after transfection, cells are washed once with phosphate buffered saline (PBS)
15 pre-warmed to 37°C. Serum-free α MEM is then added to the cells either alone (control) or with one or more candidate modulators and the cells are incubated at 37°C for five hours. Thereafter, cells are washed once with ice cold PBS and lysed by the addition of 100 μ l of lysis buffer/well (from luciferase assay kit, Promega, Madison, WI). After incubation for 15 minutes at room temperature, 15 μ l of the
20 lysate is mixed with 50 μ l substrate solution (Promega) in an opaque white 96-well plate, and the luminescence is read immediately on a Wallace model 1450 MicroBeta scintillation and luminescence counter (Wallace Instruments, Gaithersburg, MD).

Differences in luminescence in the presence versus the absence of a candidate modulator compound are indicative of modulatory activity. Receptors that
25 are either constitutively active or activated by agonists give a 3-20 fold stimulation of luminescence compared to cells transfected with the reporter gene alone. Modulators that act as inverse agonists will reverse this effect.

D. Intracellular Calcium Measurement using FLIPR

30 Changes in intracellular calcium levels are another recognized indicator of G protein-coupled receptor activity, and such assays can be employed to

evaluate modulators of GPCR activity. For example, CHO cells stably transfected with a GPCR expression vector are plated at a density of 4×10^4 cells/well in Packard black-walled 96-well plates specially designed to isolate fluorescent signal to individual wells. The cells are incubated for 60 minutes at 37°C in modified
5 Dulbecco's PBS (D-PBS) containing 36 mg/L of pyruvate and 1 g/L of glucose with the addition of 1% FBS and one of four calcium indicator dyes (Fluo-3™ AM, Fluo-4™ AM, Calcium Green™-1 AM, or Oregon Green™ 488 BAPTA-1 AM) at a concentration of 4 µM. Plates are washed once with modified D-PBS without 1% FBS and incubated for 10 minutes at 37°C to remove residual dye from the cellular
10 membrane. In addition, a series of washes with modified D-PBS without 1% FBS is performed immediately prior to activation of the calcium response.

Calcium response is initiated by the addition of one or more candidate receptor agonist compounds, calcium ionophore A23187 (10 µM), or ATP (4 µM). Fluorescence is measured by Molecular Device's FLIPR with an argon laser,
15 excitation at 488 nm. [See, e.g., Kuntzweiler *et al.*, *Drug Development Research*, 44(1): 14-20 (1998).] The F-stop for the detector camera was set at 2.5 and the length of exposure was 0.4 milliseconds. Basal fluorescence of cells was measured for 20 seconds prior to addition of agonist, ATP, or A23187, and was subtracted from the response signal. The calcium signal is measured for approximately 200 seconds,
20 taking readings every two seconds. Calcium ionophore and ATP increase the calcium signal 200% above baseline levels. In general, activated orphan GPCRs increase the calcium signal approximately 10-15% above baseline signal.

E. Mitogenesis Assay

25 In mitogenesis assays, the ability of candidate modulators to induce or inhibit GPCR-mediated cell growth is determined. [See, e.g., Lajiness *et al.*, *Journal of Pharmacology and Experimental Therapeutics*, 267(3): 1573-81 (1993).]

For example, CHO cells stably expressing a GPCR are seeded into 96-well plates at a density of 5000 cells/well and grown at 37°C in αMEM supplemented
30 with 10% fetal calf serum. After 48 hours, the cells are rinsed twice with serum-free αMEM and 80 µl of fresh αMEM, or αMEM containing a known mitogen, is added

- 125 -

along with 20 μ l α MEM containing varying concentrations of one or more test compounds diluted in serum free media. As controls, some wells on each plate receive serum-free media alone, and some receive media containing 10% FBS.

Untransfected cells or cells transfected with vector alone also may serve as controls.

5 After culture for 16-18 hours, 1 μ Ci/well of [3 H]-thymidine (2 Ci/mmol; cpm) is added to the wells and cells are incubated for an additional 2 hours at 37°C. The cells are trypsinized and harvested onto filter mats with a cell harvester (Tomtec) and the filters are counted in a Betaplate counter. The incorporation of 3 H-thymidine in serum-free test wells is compared to the results achieved in cells
10 stimulated with serum. Use of multiple concentrations of test compounds permits creation and analysis of dose-response curves using the non-linear, least squares fit equation: $A = B \times [C / (D + C)] + G$ where A is the percent of serum stimulation; B is the maximal effect minus baseline; C is the EC_{50} ; D is the concentration of the compound; and G is the maximal effect. Parameters B, C and G are determined by
15 Simplex optimization.

Agonists that bind to the receptor are expected to increase [3 H]-thymidine incorporation into cells, showing up to 80% of the response to serum. Antagonists that bind to the receptor will inhibit the stimulation seen with a known agonist by up to 100%.

20 F. [35 S]GTP γ S Binding Assay

Because G protein-coupled receptors signal through intracellular "G proteins" whose activity involves GTP/GDP binding and hydrolysis. Another indicator of GPCR modulator activity is measuring binding of the non-hydrolyzable
25 GTP analog [35 S]GTP γ S in the presence and absence of putative modulators. [See, *e.g.*, Kowal, *et al.*, *Neuropharmacology*, 37: 179-87 (1998).]

In one exemplary assay, cells stably transfected with a GPCR expression vector are grown in 10 cm dishes to subconfluence, rinsed once with 5 ml of ice cold Ca^{2+} /Mg $^{2+}$ free PBS, and scraped into 5 ml of the same buffer. Cells are
30 pelleted by centrifugation (500 x g, 5 minutes), resuspended in TEE buffer (25 mM Tris, 5 mM EDTA, 5 mM EGTA, pH 7.5) and frozen in liquid nitrogen. After

- 126 -

thawing, the cells are homogenized using a dounce (one ml TEE per plate of cells), and centrifuged at 1,000 x g for 5 minutes to remove nuclei and unbroken cells.

The homogenate supernatant is centrifuged at 20,000 x g for 20 minutes to isolate the membrane fraction. The membrane pellet is then washed once with TEE and resuspended in binding buffer (20 mM HEPES, pH 7.5, 150 mM NaCl, 10 mM MgCl₂, 1 mM EDTA). The resuspended membranes can be frozen in liquid nitrogen and stored at -70°C until use.

Aliquots of cell membranes prepared as described above and stored at -70°C are thawed, homogenized, and diluted to a concentration of 10-50 µg/ml in buffer containing 20 mM HEPES, 10 mM MgCl₂, 1 mM EDTA, 120 mM NaCl, 10 µM GDP, and 0.2 mM ascorbate. In a final volume of 90 µl, homogenates are incubated with varying concentrations of putative modulator compounds or 100 µM GTP for 30 minutes at 30°C and then placed on ice. To each sample, 10 µl guanosine 5'-O-(3[³⁵S]thio) triphosphate (NEN, 1200 Ci/mmol), ([³⁵S]-GTPγS), was added to a final concentration of 100-200 pM. Samples are incubated at 30°C for an additional 30 minutes. The reaction is then stopped by the addition of 1 ml of 10 mM HEPES, and 10 mM MgCl₂ (pH 7.4), at 4°C, and filtration.

Samples are filtered over Whatman GF/B filters. These filters are washed with 20 ml ice-cold 10 mM HEPES (pH 7.4) and 10 mM MgCl₂ and counted by liquid scintillation spectroscopy. Nonspecific binding of [³⁵S]-GTPγS is measured in the presence of 100 µM GTP and subtracted from the total. Compounds are selected that modulate the amount of [³⁵S]-GTPγS binding in the cells, compared to untransfected control cells. Activation of receptors by agonists gives up to a five-fold increase in [³⁵S]GTPγS binding. This response is blocked by antagonists.

G. MAP Kinase Activity Assay

Evaluation of MAP Kinase activity in cells expressing a GPCR provide another assay to identify modulators of GPCR activity. [See, e.g., Lajiness *et al.*, *Journal of Pharmacology and Experimental Therapeutics*, 267(3): 1573-81 (1993); and Boulton *et al.*, *Cell*, 65: 663-75 (1991).]

- 127 -

In one embodiment, CHO cells stably transfected with a GPCR-encoding polynucleotide are seeded into 6 well plates at a density of 70,000 cells/well 48 hours prior to the assay. During this time, the cells are cultured at 37°C in α MEM media supplemented with 10% FBS, 2 mM glutamine, 10 U/ml penicillin and 10 μ g/ml streptomycin. The cells are serum starved for 1-2 hours prior to the addition of
5 stimulants.

For the assay, the cells are treated with media alone or media containing a putative agonist or phorbol ester-myristoyl acetate (PMA) as a positive control. After treatment, cells are incubated at 37°C for varying times. To stop the
10 reaction, the plates are placed on ice, the media is aspirated, and the cells are rinsed with 1 ml of ice-cold PBS containing 1 mM EDTA. Thereafter, 200 μ l cell lysis buffer (12.5 mM MOPS (pH 7.3), 12.5 mM β -glycerophosphate, 7.5 mM $MgCl_2$, 0.5 mM EGTA, 0.5 mM sodium vanadate, 1 mM benzamidine, 1 mM dithiothreitol, 10 μ g/ml leupeptin, 10 μ g/ml aprotinin, 2 μ g/ml pepstatin A, and 1 μ M okadaic acid) is
15 added to the cells. The cells are scraped from the plates and homogenized by 10 passages through a 23 3/4 gauge needle. The cytosol fraction is prepared by centrifugation at 20,000 x g for 15 minutes.

Aliquots (5-10 μ l containing 1-5 μ g protein) of cytosols are mixed with 1 mM MAPK Substrate Peptide (APRTPGGRR; SEQ ID NO: 25); Upstate
20 Biotechnology, Inc., N.Y.) and 50 μ M [γ - ^{32}P]ATP, (NEN, 3000 Ci/mmol) diluted to a final specific activity of ~2000 cpm/pmol in a total volume of 25 μ l. The samples are incubated for 5 minutes at 30°C, and reactions are stopped by spotting 20 μ l on 2 cm² of Whatman P81 phosphocellulose paper. The filter squares are washed in 4 changes of 1% H_3PO_4 , and the squares are counted by liquid scintillation spectroscopy.
25 Equivalent cytosolic extracts are incubated without MAPK substrate peptide, and the cpm from these samples are subtracted from the matched samples with the substrate peptide. The cytosolic extract from each well is used as a separate point. Protein concentrations are determined by a dye binding protein assay (Bio-Rad). Agonist activation of the receptor is expected to result in up to a five fold increase in MAPK
30 enzyme activity. This increase is blocked by antagonists.

H. [³H]Arachidonic Acid Release

The activation of GPCR's also has been observed to potentiate arachidonic acid release in cells, providing yet another useful assay for modulators of the activity of GPCR's of the present invention. [See, e.g., Kanterman *et al.*,
5 *Molecular Pharmacology*, 39: 364-9 (1991).] For example, CHO cells that are stably transfected with a GPCR expression vector are plated in 24-well plates at a density of 15,000 cells/well and grown in α MEM media supplemented with 10% FBS, 2 mM glutamine, 10 U/ml penicillin and 10 μ g/ml streptomycin for 48 hours at 37°C before use. Cells of each well are labeled by incubation with [³H]arachidonic acid
10 (Amersham Corp., 210 Ci/mmol) at 0.5 μ Ci/ml in 1 ml α MEM supplemented with 10 mM HEPES (pH 7.5), and 0.5% fatty-acid-free bovine serum albumin for 2 hours at 37°C. The cells are then washed twice with 1 ml of the same buffer.

Candidate modulator compounds are added in 1 ml of the same buffer, either alone or containing 10 μ M ATP (Adenosine 5'-triphosphate) and the cells are
15 incubated at 37°C for 30 minutes. Buffer alone and mock transfected cells are used as controls. Samples (0.5 ml) from each well are counted by liquid scintillation spectroscopy. Agonists which activate the receptor will lead to potentiation of the ATP-stimulated release of [³H]-arachidonic acid. This potentiation is blocked by antagonists.

20

I. Extracellular Acidification Rate

In yet another assay, the effects of putative modulators of GPCR activity are assayed by monitoring extracellular changes in pH induced by the putative modulators. [See, e.g., Dunlop *et al.*, *Journal of Pharmacological and Toxicological*
25 *Methods*, 40(1): 47-55 (1998).]

CHO cells transfected with a GPCR expression vector are seeded into 12-mm capsule cups (Molecular Devices Corp.) at 4×10^5 cells/cup in α MEM supplemented with 10% FBS, 2 mM l-glutamine, 10 units/ml penicillin, and 10 μ g/ml streptomycin. The cells are incubated in this media at 37°C in 5% CO₂ for 24 hours.

30 Extracellular acidification rates are measured using a Cytosensor microphysiometer (Molecular Devices Corp.). The capsule cups are loaded into the

- 129 -

sensor chambers of the microphysiometer and the chambers are perfused with running buffer (bicarbonate free α MEM supplemented with 4 mM L-glutamine, 10 units/ml penicillin, 10 μ g/ml streptomycin, 26 mM NaCl) at a flow rate of 100 μ l/min.

Agonists or other agents are diluted into the running buffer and perfused through a second fluid path. During each 60 second pump cycle, the pump is run for 38 seconds and is off for the remaining 22 seconds. The pH of the running buffer in the sensor chamber is recorded during the cycle from 43-58 seconds, and the pump is re-started at 60 seconds to start the next cycle. The rate of acidification of the running buffer during the recording time is calculated by the Cytosoft program. Changes in the rates of acidification are calculated by subtracting the baseline value (the average of 4 rate measurements immediately before addition of modulator candidates) from the highest rate measurement obtained after addition of a modulator candidate. The selected instrument detects 61 mV/pH unit. Modulators that act as agonists at the receptor result in an increase in the rate of extracellular acidification as compared to the rate in the absence of agonist. This response is blocked by modulators which act as antagonists at the receptor.

EXAMPLE 7

Luciferase Reporter Gene Assays

Luciferase reporter gene assays (essentially as described in Example 6) were carried out to measure signaling activity of the GPCR receptors when coupled to Gs, Gi or Gq G-proteins. Activation of Gs coupled receptors results in stimulation of intracellular cAMP production which leads to activation of the transcription factor cyclic AMP response element (CRE). Therefore activation of Gs coupled receptors can be detected by measuring transcription and translation of the reporter gene CRE-luciferase. The level of expression of the CRE reporter gene is dependent on the intracellular level of cAMP. Similarly, activation of Gs, Gi or Gq coupled receptors will result in activation of the AP-1 transcription factor. Expression of the AP-1 transcription factor can be attributed to changes in cAMP levels and/or increases in the levels of intracellular calcium and therefore can be an indication of G-protein coupled receptor activation.

- 130 -

CHO 10001A cells (Gottesman *et al.*, *Somatic Cell Genetics* 6: 45-61, 1980) were maintained in Minimal Essential Medium (MEM) supplemented with 10% FBS (Hyclone Laboratories, Inc., Logan, Utah) at 37°C in an atmosphere of 5% CO₂. The cells were split 1:5 twice a week for maintenance. Plasmids used in the experiments were propagated in *E. coli* strain DH5 (Gibco BRL) and purified using the Qiagen Maxi-prep plasmid purification system according to the manufacturer's instructions.

One day prior to transfection, 1×10^5 CHO cells/well were plated on 24 well culture plates and allowed to adhere overnight. Each well on the plate was transfected with 0.5 µg of either AP-1 luciferase (Stratagene, LaJolla, CA) or CRE luciferase plasmid alone or in combination with 0.125 µg of a GPCR plasmid (GPCR DNA inserted into the pCDNA3 vector from Invitrogen). Cells were transiently transfected with the commercially available transfection reagent FUGENE-6 according to the manufacturer's instructions (Boehringer Mannheim, Indianapolis, IN).

Twenty-four hours after transfection, the cells were washed in PBS pre-warmed to 37°C. Agonists and antagonists were diluted in pre-warmed serum-free MEM, added to the transfected cells and incubated at 37°C, 5% CO₂ for 5 hours. Subsequently, the cells were washed once in ice cold PBS and lysed with the addition of 100 µl of lysis buffer (Promega) to each well. After a 15 minute incubation at room temperature, luciferase reporter gene activation was analyzed with the Luciferase Assay Reagents commercially available from Promega (Madison, WI). An aliquot of lysate (15 µl) was mixed with 50 µl of substrate solution in an opaque white 96 well plate. The luminescence from the plate was read in a Wallance 1450 MicroBeta scintillation and luminescence counter (Wallac Instruments, Gaithersburg, MD). Constitutive GPCR activity was calculated as activity measured in GPCR transfected cells divided by activity measured in control cells (control cells= luciferase-transfected cells in the absence of GPCR plasmid). The measurements of GPCR constitutive activity (as a percentage of control measurements) are summarized in the table below:

- 131 -

	<u>GPCR</u>	<u>CRE Activity</u>	<u>AP-1 Activity</u>
	CON193	128%	100%
	CON197	165%	100%
	CON198	178%	146%
5	CON203	100%	468%
	CON215	173%	307%
	CON222	100%	100%
	CON202	135%	336%
	CON166	115%	100%
10	CON217	211%	100%

These results provide useful information for designing screening assays to identify molecules (natural or artificial) that activate or inhibit the GPCR's of the invention. For example, compound libraries can be screened using the AP-1 luciferase (for CON198, CON203, CON215, or CON202) or the CRE-luciferase assay (for CON193, CON197, CON198, CON215, CON202, and CON166) to identify compounds which increase the signaling activity in GPCR polypeptide expressing cells as compared to receptor negative cells. The identified compounds may be useful for predicting endogenous ligands for the GPCR polypeptides, for measuring the physiological effects of GPCR activation in animal models, and for designing therapeutics to modulate GPCR activity to treat disease states.

EXAMPLE 8

Chromosomal Localization of GPCR

The following example pertains to chromosomal localization of GPCR genes of the present invention (e.g., CON193, CON166, CON103, CON203, CON198, CON197, CON202, CON222, CON215, or CON217). The chromosomal localization permits use of the GPCR polynucleotide sequences (including fragments thereof) as chromosomal markers to assist with genome mapping and to provide markers for disease states. Chromosomal localization also permits correlation of the

- 132 -

GPCR's of the invention with disease states in which aberrant activity of the GPCR is implicated, especially disease states that have previously linked (or will be linked) with mutations, polymorphisms, chromosomal rearrangements, and other chromosomal changes near the locus of the GPCR gene.

5

A. CON197

Chomosomal localization of the gene encoding CON197 (SEQ ID NO: 11) was determined using the Stanford G3 Radiation Hybrid Panel (Research Genetics, Inc. Huntsville, AL). This panel contains 83 radiation hybrid clones of the entire human genome as created by the Stanford Human Genome Center (Stanford, California). PCR was carried out with each clone within the Hybrid Panel and the results were submitted to the Stanford Human Genomic Center via e-mail for analysis (<http://www.shgc.stanford.edu/RH/rhserverformnew.html>).

PCR reactions were carried out with the Expand Hi-Fi PCR System™ according the manufacturer's instructions (Roche Molecular Biochemicals, Indianapolis, IN). Primers, synthesized by Genosys Corp. (The Woodlands, TX), were designed to generate a 10 base pair fragment of CON197-encoding DNA in the presence of the appropriate genomic DNA. The forward primer, denoted as LW1332 (TCCTACTGTCATGAACCC; SEQ ID NO: 74), corresponded to nucleotides 396 through 413 of SEQ ID NO: 11. The reverse primer, denoted as LW1333 (CAGAAGAAGTTGTCCAGC; SEQ ID NO: 75), corresponded to the complement of nucleotides 519 through 536 of SEQ ID NO: 11. Each reaction contained 25 ng of DNA from a hybrid clone, 60 ng of Primer LW1332, and 60 ng of Primer LW1333 resulting in a final volume of 15 µl. The PCR reactions were carried out in a GeneAmp 9700 PCR thermocycler (Perkin Elmer Applied Biosystems) under the following conditions: 94°C for 3 minutes followed by 35 cycles of 94°C for 30 seconds, 52°C for 1 minute, and 72°C for 2 minutes. The PCR reactions were then analyzed on a 2.0% agarose gel and stained with ethidium bromide. The lanes were scored for the presence of the 140 base pair PCR product.

The G3 Hybrid Panel analysis revealed that the CON197 gene (SEQ ID NO: 11) was localized to chromosome 14, most nearly linked to Stanford marker

- 133 -

SHGC-10764 with a LOD score of 9.10. The SHGC-10764 marker lies at position 1q11.1.

B. CON202

5 Chomosomal localization of the gene encoding CON202 (SEQ ID NO: 13) was determined using the Stanford G3 Radiation Hybrid Panel (Research Genetics, Inc. Huntsville, AL). This panel contains 83 radiation hybrid clones of the entire human genome as created by the Stanford Human Genome Center (Stanford, California). PCR was carried out with each clone within the Hybrid Panel and the
10 results were submitted to the Stanford Human Genomic Center via e-mail for analysis (<http://www.shgc.stanford.edu/RH/rhserverformnew.html>).

 PCR reactions were carried out with the Expand Hi-Fi PCR System™ according to the manufacturer's instructions (Roche Molecular Biochemicals, Indianapolis, IN). Primers, synthesized by Genosys Corp. (The Woodlands, TX),
15 were designed to generate a 250 base pair fragment of CON202-encoding DNA in the presence of the appropriate genomic DNA. The forward primer, denoted as LW1480 (GGTCTACCTGGACTTATGG; SEQ ID NO: 70), corresponded to nucleotides 515 through 534 of SEQ ID NO: 13. The reverse primer, denoted as LW1481 (TAATGAATGAGTAAGTGCCC; SEQ ID NO: 71), corresponded to the
20 complement of nucleotides 745 through 764 of SEQ ID NO: 13. Each reaction contained 25 ng of DNA from a hybrid clone, 60 ng of Primer LW1480, and 60 ng of Primer LW1481 resulting in a final volume of 15 µl. The PCR reactions were carried out in a GeneAmp 9700 PCR thermocycler (Perkin Elmer Applied Biosystems) under the following conditions: 94°C for 3 minutes followed by 35 cycles of 94°C for 30
25 seconds, 52°C for 1 minute, and 72°C for 2 minutes. The PCR reactions were then analyzed on a 2.0% agarose gel and stained with ethidium bromide. The lanes were scored for the presence of the 250 base pair PCR product.

 The G3 Hybrid Panel analysis revealed that the CON202 gene (SEQ ID NO: 13) was localized to chromosome 7, most nearly linked to Stanford marker
30 SHGC-12021 with a LOD score of 10.36. The SHGC-12021 marker lies at position 7q21. There is evidence that schizophrenia is linked to chromosome 7q22, and

- 134 -

therefor any genes localized to this region are candidates for disease involvement or susceptibility. [See Ekelund *et al.*, *Human Mol. Genetics* 9(7): 1049-1057 (2000); Faraone *et al.*, *Am. J. Med. Genet.* 81: 290-295 (September, 1998); and Blouin *et al.*, *Nat. Genet.*, 20: 70-73 (1998)]. The SHGC-12021 marker is proximal to 7q22 (~1 cM) and therefore may be associated with schizophrenia susceptibility.

In particular, G protein-coupled receptors, such as CON202 polypeptide, have the biochemical and functional potential to play a role in the disease process of schizophrenia. CON202 is an attractive target for screening for ligands (natural and synthetic) that are useful in modulating cellular processes involved in schizophrenia. In addition, the chromosomal localization data (especially coupled with CON202 expression patterns in the brain) identifies CON202 as a candidate for screening healthy and affected (schizophrenia) individuals for CON202 allelic variants, mutations, duplications, rearrangements, and other chromosomal variations that correlate with the disease state. Variations that correlate with disease state are useful for diagnosis of disease or disease susceptibility. CON202 constructs containing the variations are useful for designing targeted therapeutics for treatment of the disease (e.g., by using the assays for modulators described in preceding examples.

C. High throughput Analysis

The EMBL High Throughput Genome database (provided by the European Bioinformatics Institute) was searched with GPCR nucleotide sequences to determine chromosomal localization for CON193, CON166, CON103, CON203, CON198, and CON215 genes. The results are summarized in the table below:

- 135 -

	<u>GPCR</u>	<u>SEQ ID NO:</u>	<u>Chromosome Localization</u>	<u>Based on Genbank Accession No.</u>
	CON193	1	11	AC026090
	CON166	3	X	AC021992
	CON103	5	2	AC013396
5	CON203	7	3	AC024886
	CON198	9	11	AC025249
	CON215	17	3	AC024886

While the present invention has been described in terms of specific
 10 embodiments, it is understood that variations and modifications will occur to those in
 the art, all of which are intended as aspects of the present invention. Accordingly,
 only such limitations as appear in the claims should be placed on the invention.

Summary of Sequences:

15	<u>SEQ ID NO.</u>	<u>Description</u>
	1	CON 193 DNA
	2	CON 193 protein
	3	CON 166 DNA
	4	CON 166 protein
20	5	CON 103 DNA
	6	CON 103 protein
	7	CON 203 DNA
	8	CON 203 protein
	9	CON 198 DNA
25	10	CON 198 protein
	11	CON 197 DNA
	12	CON 197 protein
	13	CON 202 DNA
	14	CON 202 protein
30	15	CON 222 DNA
	16	CON 222 protein
	17	CON 215 DNA

- 136 -

	<u>SEQ ID NO.</u>	<u>Description</u>
	18	CON 215 protein
	19	CON 217 DNA
	20	CON 217 protein
	21	PCR primer LW 1282 for CON 193
5	22	PCR primer LW 1283 for CON 193
	23	PCR primer LW 1372 for CON 193
	24	PCR primer LW 1374 for CON 193
	25	MAPK Substrate Peptide
	26	Primer LW 1248 for CON 193 to generate insitu hybridization probe
10	27	Primer LW 1249 for CON 193 to generate insitu hybridization probe
	28	PCR primer LW 1278 for CON 166
	29	PCR primer LW 1279 for CON 166
	30	PCR primer LW 1405 for CON 166
	31	PCR primer LW 1406 for CON 166
15	32	PCR primer LW 1280 for CON 103
	33	PCR primer LW 1281 for CON 103
	34	PCR primer LW 1385 for CON 103
	35	PCR primer LW 1386 for CON 103
	36	PCR primer LW 1329 for CON 203
20	37	PCR primer LW 1377 for CON 203
	38	PCR primer LW 1387 for CON 203
	39	PCR primer LW 1388 for CON 203
	40	Primer LW 1314 for CON 203 to generate insitu hybridization probe
	41	Primer LW 1315 for CON 203 to generate insitu hybridization probe
25	42	PCR primer LW 1326 for CON 198
	43	PCR primer LW 1327 for CON 198
	44	PCR primer LW 1415 for CON 198
	45	PCR primer LW 1416 for CON 198
	46	Primer LW 1308 for CON 198 to generate insitu hybridization probe
30	47	Primer LW 1309 for CON 198 to generate insitu hybridization probe
	48	PCR primer LW 1324 for CON 197
	49	PCR primer LW 1325 for CON 197
	50	Primer LW 1306 for CON 197 to generate insitu hybridization probe
	51	Primer LW 1307 for CON 197 to generate insitu hybridization probe

- 137 -

	<u>SEQ ID NO.</u>	<u>Description</u>
	52	PCR primer GV 599 for CON 202
	53	PCR primer GV 600 for CON 202
	54	PCR primer LW 1482 for CON 202
	55	PCR primer LW 148 for CON 202
5	56	Primer LW 1310 for CON 202 to generate insitu hybridization probe
	57	Primer LW 1311 for CON 202 to generate insitu hybridization probe
	58	PCR primer LW 1442 for CON 222
	59	PCR primer LW 1443 for CON 222
	60	PCR primer LW 1440 for CON 222
10	61	PCR primer LW 1441 for CON 222
	62	Primer LW 1472 for CON 222 to generate insitu hybridization probe
	63	Primer LW 1473 for CON 222 to generate insitu hybridization probe
	64	Primer LW 1411 for CON 215 to generate insitu hybridization probe
	65	Primer LW 1412 for CON 215 to generate insitu hybridization probe
15	66	PCR primer LW 1448 for CON 217
	67	PCR primer LW 1449 for CON 217
	68	Primer LW 217A for CON 217 to generate insitu hybridization probe
	69	Primer LW 218B for CON 217 to generate insitu hybridization probe
	70	Primer LW 1480 for CON 202 chromosomal localization
20	71	Primer LW 1481 for CON 202 chromosomal localization
	72	Primer CON103a for CON 103 to generate insitu hybridization probe
	73	Primer CON103b for CON 103 to generate insitu hybridization probe
	74	Primer LW 1332 for CON 197 chromosomal localization
	75	Primer LW 1333 for CON 197 chromosomal localization

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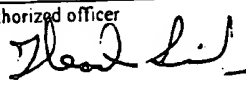
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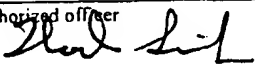
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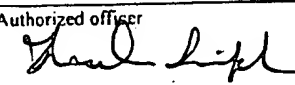
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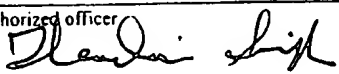
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Applicant's or agent's file reference number	28341/62/6P	International application I To Be I
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>94: 98</u> , line <u>3-7: 19</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input checked="" type="checkbox"/>	
Name of depositary institution Agricultural Research Service Culture Collection	
Address of depositary institution (including postal code and country) National Center for Agricultural Utilization Research Agricultural Research Service, U.S. Department of Agriculture 1815 North University Street, Peoria, Illinois 61604 U.S. A.	
Date of deposit 18 January 2000	Accession Number B-30252
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input checked="" type="checkbox"/>	
When designating Australia, in accordance with regulation 3.25 of the Patents Regulations (Australia Statutory Rules 1991 No. 71), samples of materials deposited in accordance with the Budapest Treaty in relation to this Patent Request are only to be provided before: the patent is granted on the application; or the application has lapsed or been withdrawn or refused; to a person who is: a skilled addressee without an interest in the invention; and nominated by a person who makes a request for the furnishing of those samples.	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications e.g. "Accession Number of Deposit")	

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Applicant's or agent's file reference number 28341/b2/b1	International application No. To Be Determined
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>94; 98</u> , line <u>3-7; 19</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input checked="" type="checkbox"/>	
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Date of deposit 18 January 2000	Accession Number B-30252
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input checked="" type="checkbox"/>	
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E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications e.g., "Accession Number of Deposit")	

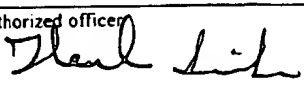
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Applicant's or agent's file reference number	2834 1/52/51	International application N To E
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>94; 98</u> , line <u>27-31; 20</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input checked="" type="checkbox"/>	
Name of depositary institution Agricultural Research Service Culture Collection	
Address of depositary institution (including postal code and country) National Center for Agricultural Utilization Research Agricultural Research Service, U.S. Department of Agriculture 1815 North University Street, Peoria, Illinois 61604 U.S. A.	
Date of deposit 18 January 2000	Accession Number B-30251
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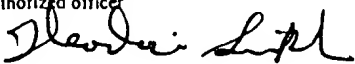
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Applicant's or agent's file reference number 28341/b2/bP	International application N To Be Del
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13b/s)

A. The indications made below relate to the microorganism referred to in the description on page 94; 98, line 27-31; 20	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input checked="" type="checkbox"/>	
Name of depositary institution Agricultural Research Service Culture Collection	
Address of depositary institution (including postal code and country) National Center for Agricultural Utilization Research Agricultural Research Service, U.S. Department of Agriculture 1815 North University Street, Peoria, Illinois 61604 U.S.A.	
Date of deposit 18 January 2000	Accession Number B-30251
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input checked="" type="checkbox"/>	
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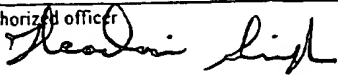
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Applicant's or agent's file reference number 2834	International application To Be Determined
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>95; 98</u> , line <u>19-23; 21</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input checked="" type="checkbox"/>	
Name of depositary institution Agricultural Research Service Culture Collection	
Address of depositary institution (including postal code and country) National Center for Agricultural Utilization Research Agricultural Research Service, U.S. Department of Agriculture 1815 North University Street, Peoria, Illinois 61604 U.S. A.	
Date of deposit 18 January 2000	Accession Number B-30253
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input checked="" type="checkbox"/>	
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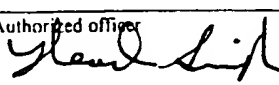
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>95; 98</u> , line <u>19-23; 21</u>	
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Name of depositary institution Agricultural Research Service Culture Collection	
Address of depositary institution (including postal code and country) National Center for Agricultural Utilization Research Agricultural Research Service, U.S. Department of Agriculture 1815 North University Street, Peoria, Illinois 61604 U.S.A.	
Date of deposit 18 January 2000	Accession Number B-30253
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input checked="" type="checkbox"/>	
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>96: 98</u> , line <u>11-15: 22</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input checked="" type="checkbox"/>	
Name of depositary institution Agricultural Research Service Culture Collection	
Address of depositary institution (including postal code and country) National Center for Agricultural Utilization Research Agricultural Research Service, U.S. Department of Agriculture 1815 North University Street, Peoria, Illinois 61604 U.S. A.	
Date of deposit 18 January 2000	Accession Number B-30257
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input checked="" type="checkbox"/>	
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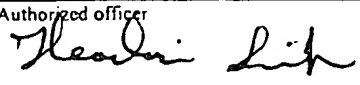
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>96; 98</u> , line <u>11-15; 22</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input checked="" type="checkbox"/>	
Name of depositary institution Agricultural Research Service Culture Collection	
Address of depositary institution (including postal code and country) National Center for Agricultural Utilization Research Agricultural Research Service, U.S. Department of Agriculture 1815 North University Street, Peoria, Illinois 61604 U.S.A.	
Date of deposit 18 January 2000	Accession Number B-30257
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input checked="" type="checkbox"/>	
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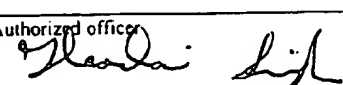
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>97; 98</u> , line <u>4-8; 23</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input checked="" type="checkbox"/>	
Name of depositary institution Agricultural Research Service Culture Collection	
Address of depositary institution (including postal code and country) National Center for Agricultural Utilization Research Agricultural Research Service, U.S. Department of Agriculture 1815 North University Street, Peoria, Illinois 61604 U.S. A.	
Date of deposit 18 January 2000	Accession Number B-30255
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input checked="" type="checkbox"/>	
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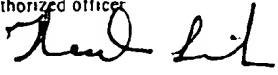
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Applicant's or agent's file reference number	28341/6276P	International To Be Det
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>97; 98</u> , line <u>4-8; 23</u>	
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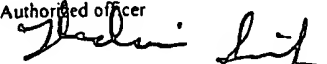
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>98</u> , line <u>1-3; 24</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input checked="" type="checkbox"/>	
Name of depositary institution Agricultural Research Service Culture Collection	
Address of depositary institution (including postal code and country) National Center for Agricultural Utilization Research Agricultural Research Service, U.S. Department of Agriculture 1815 North University Street, Peoria, Illinois 61604 U.S. A.	
Date of deposit 18 January 2000	Accession Number B-30256
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>98</u> line <u>1-3; 24</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input checked="" type="checkbox"/>	
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CLAIMS

What is claimed is:

1. A purified and isolated seven transmembrane receptor polypeptide comprising an amino acid sequence at least 90% identical to an amino acid sequence set forth in any one of SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18 or 20, or a fragment thereof comprising an epitope specific to said seven transmembrane receptor polypeptide.
2. A purified and isolated seven transmembrane receptor polypeptide according to claim 1 comprising an amino acid sequence at least 90% identical to the amino acid sequence set forth in SEQ ID NO: 2, or a fragment thereof comprising an epitope specific to said seven transmembrane receptor polypeptide.
3. A purified and isolated seven transmembrane receptor polypeptide according to claim 1 comprising an amino acid sequence at least 90% identical to the amino acid sequence set forth in SEQ ID NO: 4, or a fragment thereof comprising an epitope specific to said seven transmembrane receptor polypeptide.
4. A purified and isolated seven transmembrane receptor polypeptide according to claim 1 comprising an amino acid sequence at least 90% identical to the amino acid sequence set forth in SEQ ID NO: 6, or a fragment thereof comprising an epitope specific to said seven transmembrane receptor polypeptide.
5. A purified and isolated seven transmembrane receptor polypeptide according to claim 1 comprising an amino acid sequence at least 90% identical to the amino acid sequence set forth in SEQ ID NO: 8, or a fragment thereof comprising an epitope specific to said seven transmembrane receptor polypeptide.

6. A purified and isolated seven transmembrane receptor polypeptide according to claim 1 comprising an amino acid sequence at least 90% identical to the amino acid sequence set forth in SEQ ID NO: 10, or a fragment thereof comprising an epitope specific to said seven transmembrane receptor polypeptide.

5

7. A purified and isolated seven transmembrane receptor polypeptide according to claim 1 comprising an amino acid sequence at least 90% identical to the amino acid sequence set forth in SEQ ID NO: 12, or a fragment thereof comprising an epitope specific to said seven transmembrane receptor polypeptide.

10

8. A purified and isolated seven transmembrane receptor polypeptide according to claim 1 comprising an amino acid sequence at least 90% identical to the amino acid sequence set forth in SEQ ID NO: 14, or a fragment thereof comprising an epitope specific to said seven transmembrane receptor polypeptide.

15

9. A purified and isolated seven transmembrane receptor polypeptide according to claim 1 comprising an amino acid sequence at least 90% identical to the amino acid sequence set forth in SEQ ID NO: 16, or a fragment thereof comprising an epitope specific to said seven transmembrane receptor polypeptide.

20

10. A purified and isolated seven transmembrane receptor polypeptide according to claim 1 comprising an amino acid sequence at least 90% identical to the amino acid sequence set forth in SEQ ID NO: 18, or a fragment thereof comprising an epitope specific to said seven transmembrane receptor polypeptide.

25

11. A purified and isolated seven transmembrane receptor polypeptide according to claim 1 comprising an amino acid sequence at least 90% identical to the amino acid sequence set forth in SEQ ID NO: 20, or a fragment thereof comprising an epitope specific to said seven transmembrane receptor polypeptide.

30

12. A purified and isolated seven transmembrane receptor polypeptide according to any one of claims 1-11.

5 13. A purified and isolated polypeptide according to any one of claims 1-11 comprising at least one extracellular domain of the seven transmembrane receptor polypeptide.

10 14. A purified and isolated polypeptide according to any one of claims 1-11 comprising the N-terminal extracellular domain of the seven transmembrane receptor polypeptide.

15 15. A purified and isolated polypeptide according to any one of claims 1-11 comprising a seven transmembrane receptor fragment selected from the group consisting of an N-terminal extracellular domain transmembrane domains, extracellular loops connecting transmembrane domains, intracellular loops connecting transmembrane domains, a C-terminal cytoplasmic domain, and fusions thereof.

20 16. A polypeptide according to any one of claims 1-15, wherein the polypeptide further includes a heterologous tag amino acid sequence.

17. A purified and isolated polynucleotide comprising a nucleotide sequence that encodes the polypeptide of claim 16.

25 18. A purified and isolated polynucleotide comprising a nucleotide sequence that encodes a polypeptide according to any one of claims 2, 3, 4, 8 or 9.

30 19. A purified and isolated polynucleotide comprising a heterologous expression control sequence operatively linked to a nucleotide sequence that encodes a polypeptide according to any one of claims 1-16.

20. The polynucleotide according to claim 19, wherein the expression control sequence is a promoter sequence that promotes expression of said polynucleotide in an eukaryotic cell.

5 21. The polynucleotide according to claim 19, wherein the promoter is a heterologous promoter that promotes expression of the polynucleotide in a human cell.

10 22. A purified and isolated polynucleotide comprising a nucleotide sequence that encodes a mammalian seven transmembrane receptor, wherein said polynucleotide hybridizes to any one of the nucleotide sequences set forth in SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, or 19 or the non-coding strand complementary thereto, under the following hybridization conditions:

15 (a) hybridization for 16 hours at 42°C in a hybridization solution comprising 50% formamide, 1% SDS, 1 M NaCl, 10% dextran sulfate and

 (b) washing 2 times for 30 minutes at 60°C in a wash solution comprising 0.1x SSC and 1% SDS,
with the proviso that the nucleotide sequence of the polynucleotide differs from the coding sequence set forth in any one of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, or
20 19 and from its complementary strand by at least one nucleotide.

23. A polynucleotide according to claim 22 that encodes a human seven transmembrane receptor.

25 24. A vector comprising a polynucleotide according to any one of claims 17-23.

25 25. A vector according to claim 24 that is an expression vector for expressing the polynucleotide in a mammalian cell.

30

26. A host cell stably transformed or transfected with a polynucleotide according to any one of claims 17-23 in a manner allowing the expression in said host cell of the polypeptide or fragment thereof encoded by the polynucleotide.

5 27. A host cell stably transformed or transfected with a vector according to claim 24 or 25 in a manner allowing the expression in said host cell of the polypeptide or fragment thereof encoded by the polynucleotide.

10 28. A method for producing a seven transmembrane receptor polypeptide comprising the steps of growing a host cell according to claim 26 or 27 in a nutrient medium under conditions in which the host cell expresses a seven transmembrane receptor encoded by the polynucleotide.

15 29. A method according to claim 28, further comprising a step of isolating said polypeptide from said cell or said medium.

 30. A method according to claim 29, further comprising a step of isolating cell membranes from the host cell, wherein the cell membrane comprises the seven transmembrane receptor.

20

 31. An antibody specific for a polypeptide according to any one of claims 1-15.

 32. The antibody of claim 31 which is a monoclonal antibody.

25

 33. A hybridoma that produces an antibody according to claim 32.

 34. An antibody according to claim 31 that is a humanized antibody.

35. An antibody according to claim 31 that specifically binds an extracellular epitope of a seven transmembrane receptor having an amino acid sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18 or 20.

5

36. An antibody according to claim 35 that specifically binds to the amino-terminal extracellular domain of the seven transmembrane receptors.

37. A cell-free composition comprising polyclonal antibodies, wherein at least one of said antibodies is an antibody according to claim 31.

10

38. An anti-idiotypic antibody specific for an antibody according to claim 31.

15

39. A polypeptide comprising a fragment of an antibody according to claim 31, wherein said fragment and said polypeptide specifically bind to a seven transmembrane receptor having an amino acid sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18 or 20.

20

40. A polypeptide according to claim 39 that is selected from the group consisting of single chain antibodies and CDR-grafted antibodies.

41. A composition comprising a polypeptide according to any one of claims 1-16 in a pharmaceutically acceptable carrier.

25

42. A composition comprising an antibody according to any one of claims 31, 32, 34, 35, or 36, or a polypeptide according to claim 39 or 40, in a pharmaceutically acceptable carrier.

43. A method for modulating ligand binding of a seven transmembrane receptor polypeptide according to any one of claims 1-15, comprising the step of contacting said seven transmembrane receptor polypeptide with an antibody specific for said seven transmembrane receptor, under conditions wherein the antibody binds the receptor.

44. A method for modulating ligand binding of a seven transmembrane receptor polypeptide comprising the step of contacting said seven transmembrane receptor polypeptide with a polypeptide according to claim 39 or 40.

10

45. An assay to identify compounds that bind a seven transmembrane receptor polypeptide, said assay comprising the steps of:

(a) contacting a composition comprising a seven transmembrane receptor polypeptide according to any of claims 1-15 with a compound suspected of binding the seven transmembrane receptor polypeptide; and

(b) measuring binding between the compound and the seven transmembrane receptor polypeptide.

46. A method for identifying a modulator of binding between a seven transmembrane receptor polypeptide and a binding partner of the seven transmembrane receptor polypeptide, comprising the steps of:

(a) contacting the binding partner and a composition comprising the seven transmembrane receptor polypeptide in the presence and in the absence of a putative modulator compound, where the seven transmembrane receptor polypeptide is a polypeptide according to any one of claims 1-15;

(b) measuring binding between the binding partner and said seven transmembrane receptor polypeptide; and

(c) identifying a putative modulator compound in view of decreased or increased binding between the binding partner and seven transmembrane receptor polypeptide in the presence of the putative modulator, as compared to binding in the absence of the putative modulator.

30

47. An assay according to claim 45 or 46 wherein the composition comprises a cell expressing the seven transmembrane receptor polypeptide on its surface.

5 48. An assay according to claim 47 wherein the measuring step comprises measuring intracellular signaling of the seven transmembrane receptor polypeptide induced by the compound.

10 49. A method for treating a neurological disorder comprising the step of administering to a mammal in need of such treatment a pharmaceutical composition comprising a compound in an amount effective to modulate biological activity of a seven transmembrane receptor in neurons of said mammal, wherein the compound is selected from the group consisting of:

- 15 (a) an antibody according to any one of claims 31, 32, 34, 35, or 36;
 (b) an anti-idiotypic antibody according to claim 38;
 (c) a polypeptide according to claim 39 or 40;
 (d) a compound identified according to the method of claim 45; and
 (e) a modulator identified according to claim 46.

20 50. The method of claim 49 wherein the neurological disorder is schizophrenia.

25 51. A method according to claim 50, wherein the seven transmembrane receptor comprises a polypeptide according to claim 8.

30 52. A method of treating schizophrenia comprising the step of administering to a human diagnosed with schizophrenia an amount of a modulator of CON202 receptor activity sufficient to modulate CON202 receptor activity or CON202 ligand binding in said human.

53. A method of diagnosing schizophrenia or a susceptibility to schizophrenia comprising the steps of:

(a) measuring the presence or amount of expression or activity of a polypeptide according to claim 8 in a cell of a human patient; and

5 (b) comparing the measurement of step (a) to a measurement of expression or activity of the polypeptide in a cell from a normal subject or the patient at an earlier time, wherein the diagnosis of schizophrenia or susceptibility to schizophrenia is based on the presence or amount of CON202 polypeptide expression or activity.

10 54. A method of screening a human subject to diagnose a disorder affecting the brain or genetic predisposition therefor, comprising the steps of:

(a) assaying nucleic acid of a human subject to determine a presence or an absence of a mutation altering the amino acid sequence, expression, or biological activity of at least one seven transmembrane receptor that is expressed in the brain,
15 wherein the seven transmembrane receptor comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 2, 4, 6, 8, 10, 12, 14, 16, 18, and 20, or an allelic variant thereof, and wherein the nucleic acid corresponds to the gene encoding the seven transmembrane receptor; and

(b) diagnosing the disorder or predisposition from the presence or absence of
20 said mutation, wherein the presence of a mutation altering the amino acid sequence, expression, or biological activity of allele in the nucleic acid correlates with an increased risk of developing the disorder.

55. A method according to claim 54, wherein the seven
25 transmembrane receptor is CON202 comprising an amino acid sequence set forth in SEQ ID NO: 14, or an allelic variant thereof.

56. A method according to claim 55, wherein the disease is schizophrenia.

30

57. A method according to claim 56, wherein the assaying step comprises at least one procedure selected from the group consisting of:

(a) determining a nucleotide sequence of at least one codon of at least one CON202 allele of the human subject;

5 (b) performing a hybridization assay to determine whether nucleic acid from the human subject has a nucleotide sequence identical to or different from one or more reference sequences;

(c) performing a polynucleotide migration assay to determine whether nucleic acid from the human subject has a nucleotide sequence identical to or different
10 from one or more reference sequences; and

(d) performing a restriction endonuclease digestion to determine whether nucleic acid from the human subject has a nucleotide sequence identical to or different from one or more reference sequences.

15 58. A method according to claim 56 wherein the assaying step comprises: performing a polymerase chain reaction (PCR) to amplify nucleic acid comprising CON202 coding sequence, and determining nucleotide sequence of the amplified nucleic acid.

20 59. A method of screening for a CON202 hereditary schizophrenia genotype in a human patient, comprising the steps of:

(a) providing a biological sample comprising nucleic acid from said patient, said nucleic acid including sequences corresponding to said patient's CON202 alleles;

25 (b) analyzing said nucleic acid for the presence of a mutation or mutations;

(c) determining a CON202 genotype from said analyzing step; and

(d) correlating the presence of a mutation in a CON202 allele with a hereditary schizophrenia genotype.

60. The method according to claim 59 wherein said biological sample is a cell sample.

61. The method according to claim 59 wherein said analyzing comprises sequencing a portion of said nucleic acid, said portion comprising at least one codon of said CON202 alleles.

62. The method according to claim 59 wherein said nucleic acid is DNA.

63. The method according to claim 59 wherein said nucleic acid is RNA.

64. A kit for screening a human subject to diagnose schizophrenia or a genetic predisposition therefor, comprising, in association:

(a) an oligonucleotide useful as a probe for identifying polymorphisms in a human CON202 seven transmembrane receptor gene, the oligonucleotide comprising 6-50 nucleotides that have a sequence that is identical or exactly complementary to a portion of a wild type human CON202 gene sequence or CON202 coding sequence, except for one sequence difference selected from the group consisting of a nucleotide addition, a nucleotide deletion, or nucleotide substitution; and

(b) a media packaged with the oligonucleotide containing information identifying polymorphisms identifiable with the probe that correlate with schizophrenia or a genetic predisposition therefor.

65. A method of identifying a seven transmembrane allelic variant that correlates with a mental disorder, comprising steps of:

(a) providing a biological sample comprising nucleic acid from a human patient diagnosed with a mental disorder, or from the patient's genetic progenitors or progeny;

(b) analyzing said nucleic acid for the presence of a mutation or mutations in at least one seven transmembrane receptor that is expressed in the brain, wherein the at least one seven transmembrane receptor comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 2, 4, 6, 8, 10, 12, 14, 16, 18, and 20, or an allelic variant thereof, and wherein the nucleic acid includes sequence corresponding to the gene or genes encoding the at least one seven transmembrane receptor;

(c) determining a genotype for the patient for the at least one seven transmembrane receptor from said analyzing step; and

(d) identifying an allelic variant that correlates with the mental disorder from the determining step.

66. A method according to claim 65, wherein the disorder is schizophrenia, and wherein the at least one seven transmembrane receptor comprises CON202 having an amino acid sequence set forth in SEQ ID NO: 14, or an allelic variant thereof.

67. A purified and isolated polynucleotide comprising a nucleotide sequence encoding a CON202 receptor allelic variant identified according to claim 66.

68. A host cell transformed or transfected with a polynucleotide according to claim 67 or with a vector comprising the polynucleotide.

69. A purified polynucleotide comprising a nucleotide sequence encoding a CON202 seven transmembrane receptor protein of a human that is affected with schizophrenia;

wherein said polynucleotide hybridizes to the complement of SEQ ID NO: 13 under the following hybridization conditions:

(a) hybridization for 16 hours at 42°C in a hybridization solution comprising 50% formamide, 1% SDS, 1 M NaCl, 10% dextran sulfate and

(b) washing 2 times for 30 minutes at 60°C in a wash solution comprising 0.1x SSC and 1% SDS; and

wherein the polynucleotide encodes a CON202 amino acid sequence that differs from SEQ ID NO: 14 at at least one residue.

70. A vector comprising a polynucleotide according to claim 69.

71. A host cell that has been transformed or transfected with a polynucleotide according to claim 70 and that expresses the CON202 protein encoded by the polynucleotide.

72. A host cell according to claim 71 that has been co-transfected with a polynucleotide encoding the CON202 amino acid sequence set forth in SEQ ID NO: 14 and that expresses the con202 protein having the amino acid sequence set forth in SEQ ID NO: 14.

73. A method for identifying a modulator of CON202 biological activity, comprising the steps of:

a) contacting a cell according to claim 71 in the presence and in the absence of a putative modulator compound;

b) measuring CON202 biological activity in the cell; and

c) identifying a putative modulator compound in view of decreased or increased CON202 biological activity in the presence versus absence of the putative modulator.

74. An assay to identify compounds useful for the treatment of schizophrenia, said assay comprising steps of:

(a) contacting a composition comprising a seven transmembrane receptor polypeptide according to claim 8 with a compound suspected of binding the seven transmembrane receptor polypeptide;

(b) measuring binding between the compound and the seven transmembrane receptor polypeptide; and

(c) identifying molecules that bind the seven transmembrane receptor as candidate compounds useful for the treatment of schizophrenia.

75. A method for identifying compound useful for a modulator of binding between a seven transmembrane receptor polypeptide and a binding partner of the seven transmembrane receptor polypeptide, which modulator is useful for treatment of schizophrenia, comprising the steps of:

(a) contacting the binding partner and a composition comprising the seven transmembrane receptor polypeptide in the presence and in the absence of a putative modulator compound, where the seven transmembrane receptor polypeptide is a polypeptide according to claim 8;

(b) measuring binding between the binding partner and the seven transmembrane receptor polypeptide;

(c) identifying a modulator compound useful for the treatment of schizophrenia in view of decreased or increased binding between the binding partner and seven transmembrane receptor polypeptide in the presence of the putative modulator, as compared to binding in the absence of the putative modulator.

76. An assay according to claim 74 or 75 wherein the composition comprises a cell expressing the seven transmembrane receptor polypeptide on its surface.

77. An assay according to claim 76 wherein the composition comprises a cell transformed or transfected with a polynucleotide encoding the seven transmembrane polypeptide and expressing the seven transmembrane receptor polypeptide on its surface.

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Val Gly Ile Trp Ile Phe Val Ile Leu Thr Ser Ser Pro Phe Leu Met
 145 150 155 160

Ala Lys Pro Gln Lys Asp Glu Lys Asn Asn Thr Lys Cys Phe Glu Pro
 165 170 175

Pro Gln Asp Asn Gln Thr Lys Asn His Val Leu Val Leu His Tyr Val
 180 185 190

- 7 -

Ser Leu Phe Val Gly Phe Ile Ile Pro Phe Val Ile Ile Ile Val Cys
 195 200 205

Tyr Thr Met Ile Ile Leu Thr Leu Leu Lys Lys Ser Met Lys Lys Asn
 210 215 220

Leu Ser Ser His Lys Lys Ala Ile Gly Met Ile Met Val Val Thr Ala
 225 230 235 240

Ala Phe Leu Val Ser Phe Met Pro Tyr His Ile Gln Arg Thr Ile His
 245 250 255

Leu His Phe Leu His Asn Glu Thr Lys Pro Cys Asp Ser Val Leu Arg
 260 265 270

Met Gln Lys Ser Val Val Ile Thr Leu Ser Leu Ala Ala Ser Asn Cys
 275 280 285

Cys Phe Asp Pro Leu Leu Tyr Phe Phe Ser Gly Gly Asn Phe Arg Lys
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Arg Leu Ser Thr Phe Arg Lys His Ser Leu Ser Ser Val Thr Tyr Val
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Met Glu Leu His Asn Leu Ser Ser	
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Pro Ser Pro Ser Leu Ser Ser Ser Val Leu Pro Pro Ser Phe Ser Pro	
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Ser Pro Ser Ser Ala Pro Ser Ala Phe Thr Thr Val Gly Gly Ser Ser	
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Gly Gly Pro Cys His Pro Thr Ser Ser Ser Leu Val Ser Ala Phe Leu	
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gca cca atc ctg gcc ctg gag ttt gtc ctg ggc ctg gtg ggg aac agt	906
Ala Pro Ile Leu Ala Leu Glu Phe Val Leu Gly Leu Val Gly Asn Ser	
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Leu Ala Leu Phe Ile Phe Cys Ile His Thr Arg Pro Trp Thr Ser Asn	
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Thr Val Phe Leu Val Ser Leu Val Ala Ala Asp Phe Leu Leu Ile Ser	
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Asn Leu Pro Leu Arg Val Asp Tyr Tyr Leu Leu His Glu Thr Trp Arg	
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Phe Gly Ala Ala Ala Cys Lys Val Asn Leu Phe Met Leu Ser Thr Asn	
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cgc acg gcc agc gtt gtc ttc ctc aca gcc atc gca ctc aac cgc tac	1146
Arg Thr Ala Ser Val Val Phe Leu Thr Ala Ile Ala Leu Asn Arg Tyr	
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Leu Lys Val Val Gln Pro His His Val Leu Ser Arg Ala Ser Val Gly	
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Ala Ala Ala Arg Val Ala Gly Gly Leu Trp Val Gly Ile Leu Leu Leu	
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Asn Gly His Leu Leu Leu Ser Thr Phe Ser Gly Pro Ser Cys Leu Ser	
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tac agg gtg ggc acg aag ccc tcg gcc tcg ctc cgc tgg cac cag gca	1338
Tyr Arg Val Gly Thr Lys Pro Ser Ala Ser Leu Arg Trp His Gln Ala	
205 210 215	
ctg tac ctg ctg gag ttc ttc ctg cca ctg gcg ctc atc ctc ttt gct	1386
Leu Tyr Leu Leu Glu Phe Phe Leu Pro Leu Ala Leu Ile Leu Phe Ala	
220 225 230	

- 9 -

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 Ile Val Ser Ile Gly Leu Thr Ile Arg Asn Arg Gly Leu Gly Gly Gln
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gca ggc ccg cag agg gcc atg cgt gtg ctg gcc atg gtg gtg gcc gtc 1482
 Ala Gly Pro Gln Arg Ala Met Arg Val Leu Ala Met Val Val Ala Val
 250 255 260

tac acc atc tgc ttc ttg ccc agc atc atc ttt ggc atg gct tcc atg 1530
 Tyr Thr Ile Cys Phe Leu Pro Ser Ile Ile Phe Gly Met Ala Ser Met
 265 270 275 280

gtg gct ttc tgg ctg tcc gcc tgc cga tcc ctg gac ctc tgc aca cag 1578
 Val Ala Phe Trp Leu Ser Ala Cys Arg Ser Leu Asp Leu Cys Thr Gln
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 Pro Val Leu Tyr Cys Phe Ser Ser Pro Asn Phe Leu His Gln Ser Arg
 315 320 325

gcc ttg ctg ggc ctc acg cgg ggc cgg cag ggc cca gtg agc gac gag 1722
 Ala Leu Leu Gly Leu Thr Arg Gly Arg Gln Gly Pro Val Ser Asp Glu
 330 335 340

agc tcc tac caa ccc tcc agg cag tgg cgc tac cgg gag gcc tct agg 1770
 Ser Ser Tyr Gln Pro Ser Arg Gln Trp Arg Tyr Arg Glu Ala Ser Arg
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 Lys Ala Glu Ala Ile Gly Lys Leu Lys Val Gln Gly Glu Val Ser Leu
 365 370 375

gaa aag gaa ggc tcc tcc cag ggc tga gggccagctg cagggtgca 1865
 Glu Lys Glu Gly Ser Ser Gln Gly
 380 385

gcgctgtggg ggtaagggt gccgcgtct ggcttgagg gacaaggcca gcacacggtg 1925
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<212> PRT

<213> Homo sapiens

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Phe Thr Thr Val Gly Gly Ser Ser Gly Gly Pro Cys His Pro Thr Ser
 35           40           45

Ser Ser Ser Leu Val Ser Ala Phe Leu Ala Pro Ile Leu Ala Leu Glu Phe
 50           55           60

Val Leu Gly Leu Val Gly Asn Ser Leu Ala Leu Phe Ile Phe Cys Ile
 65           70           75           80

His Thr Arg Pro Trp Thr Ser Asn Thr Val Phe Leu Val Ser Leu Val
      85           90           95

Ala Ala Asp Phe Leu Leu Ile Ser Asn Leu Pro Leu Arg Val Asp Tyr
      100           105           110

Tyr Leu Leu His Glu Thr Trp Arg Phe Gly Ala Ala Ala Cys Lys Val
 115           120           125

Asn Leu Phe Met Leu Ser Thr Asn Arg Thr Ala Ser Val Val Phe Leu
 130           135           140

Thr Ala Ile Ala Leu Asn Arg Tyr Leu Lys Val Val Gln Pro His His
 145           150           155           160

Val Leu Ser Arg Ala Ser Val Gly Ala Ala Ala Arg Val Ala Gly Gly
      165           170           175

Leu Trp Val Gly Ile Leu Leu Leu Asn Gly His Leu Leu Leu Ser Thr
 180           185           190

Phe Ser Gly Pro Ser Cys Leu Ser Tyr Arg Val Gly Thr Lys Pro Ser
 195           200           205

Ala Ser Leu Arg Trp His Gln Ala Leu Tyr Leu Leu Glu Phe Phe Leu
 210           215           220

Pro Leu Ala Leu Ile Leu Phe Ala Ile Val Ser Ile Gly Leu Thr Ile
 225           230           235           240

Arg Asn Arg Gly Leu Gly Gly Gln Ala Gly Pro Gln Arg Ala Met Arg
      245           250           255

Val Leu Ala Met Val Val Ala Val Tyr Thr Ile Cys Phe Leu Pro Ser
      260           265           270

Ile Ile Phe Gly Met Ala Ser Met Val Ala Phe Trp Leu Ser Ala Cys
 275           280           285

Arg Ser Leu Asp Leu Cys Thr Gln Leu Phe His Gly Ser Leu Ala Phe
 290           295           300

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- 11 -

Thr Tyr Leu Asn Ser Val Leu Asp Pro Val Leu Tyr Cys Phe Ser Ser
305 310 315 320

Pro Asn Phe Leu His Gln Ser Arg Ala Leu Leu Gly Leu Thr Arg Gly
325 330 335

Arg Gln Gly Pro Val Ser Asp Glu Ser Ser Tyr Gln Pro Ser Arg Gln
340 345 350

Trp Arg Tyr Arg Glu Ala Ser Arg Lys Ala Glu Ala Ile Gly Lys Leu
355 360 365

Lys Val Gln Gly Glu Val Ser Leu Glu Lys Glu Gly Ser Ser Gln Gly
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cctcccaaag gtgacactgg aagca atg aac acc aca gtg atg caa ggc ttc 172
Met Asn Thr Thr Val Met Gln Gly Phe
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aac aga tct gag cgg tgc ccc aga gac act cgg ata gta cag ctg gta 220
Asn Arg Ser Glu Arg Cys Pro Arg Asp Thr Arg Ile Val Gln Leu Val
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Phe Pro Ala Leu Thr Val Val Phe Leu Thr Gly Ile Leu Leu Asn
30 35 40

act ttg gct ctg tgg gtg ttt gtt cac atc ccc agc tcc tcc acc ttc 316
Thr Leu Ala Leu Trp Val Phe Val His Ile Pro Ser Ser Thr Phe
45 50 55

atc atc tac ctg aaa aac act ttg gtg gcc gac ttg ata atg aca ctg 364
Ile Ile Tyr Leu Lys Asn Thr Leu Val Ala Asp Leu Ile Met Thr Leu
60 65 70

atg ctt cct ttc aaa atc ctg tct gac tca cac ctg gca ccc tgg cag 412
Met Leu Pro Phe Lys Ile Leu Ser Asp Ser His Leu Ala Pro Trp Gln
75 80 85

ctc aga gct ttt gtg tgt cgt ttt tct tcg gtg ata ttt tat gag acc 460
Leu Arg Ala Phe Val Cys Arg Phe Ser Ser Val Ile Phe Tyr Glu Thr
90 95 100 105

atg tat gtg ggc atc gtg ctg tta ggg ctg ata gcc ttt gac aga ttc 508
Met Tyr Val Gly Ile Val Leu Leu Gly Leu Ile Ala Phe Asp Arg Phe
110 115 120

- 12 -

ctc aag atc atc aga cct ttg aga aat att ttt cta aaa aaa cct gtt 556
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 125 130 135

ttt gca aaa acg gtc tca atc ttc atc tgg gtc ttt ttg gtc ttc atc 604
 Phe Ala Lys Thr Val Ser Ile Phe Ile Trp Val Phe Leu Val Phe Ile
 140 145 150

tcc ctg cca aat atg atc ttg agc aac aag gaa gca aca cca tcg tct 652
 Ser Leu Pro Asn Met Ile Leu Ser Asn Lys Glu Ala Thr Pro Ser Ser
 155 160 165

gtg aaa aag tgt gct tcc tta aag ggg cct ctg ggg ctg aaa tgg cat 700
 Val Lys Lys Cys Ala Ser Leu Lys Gly Pro Leu Gly Leu Lys Trp His
 170 175 180 185

caa atg gta aat aac ata tgc cag ttt att ttc tgg act ggt ttt atc 748
 Gln Met Val Asn Asn Ile Cys Gln Phe Ile Phe Trp Thr Gly Phe Ile
 190 195 200

cta atg ctt gtg ttt tat gtg gtt att gca aaa aaa gta tat gat tct 796
 Leu Met Leu Val Phe Tyr Val Val Ile Ala Lys Lys Val Tyr Asp Ser
 205 210 215

tat aga aag tcc aaa agt aag gac aga aaa aac aac aaa aag ctg gaa 844
 Tyr Arg Lys Ser Lys Ser Lys Asp Arg Lys Asn Asn Lys Lys Leu Glu
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ggc aaa gta ttt gtt gtc gtg gct gtc ttc ttt gtg tgt ttt gct cca 892
 Gly Lys Val Phe Val Val Val Ala Val Phe Phe Val Cys Phe Ala Pro
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act gac tgt aga ctg caa aat caa ctg ttt att gct aaa gaa aca act 988
 Thr Asp Cys Arg Leu Gln Asn Gln Leu Phe Ile Ala Lys Glu Thr Thr
 270 275 280

ctc ttt ttg gca gca act aac att tgt atg gat ccc tta ata tac ata 1036
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 Lys Thr Thr Ala Ser Ser Gln Glu Asn His Ser Ser Gln Thr Asp Asn
 315 320 325

ata acc tta ggc tga caactgtaca taggggtaac ttctatttat tgatgagact 1187
 Ile Thr Leu Gly
 330

tccgtagata atgtggaaat caaattttaac caagaaaaaa agattggaac aaatgctctc 1247

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tctattcata agctgaatga accattacct aagagaatgc aacaggatac caatggccac 1367

tagaggcata ttccttcttc tttttttttt gttaaatttc aagagcattc actttacatt 1427

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tggaagact aaggggaacg gttatcctac aaacctccct tcaacacctt ttacatt 1484

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35 40 45

Val His Ile Pro Ser Ser Ser Thr Phe Ile Ile Tyr Leu Lys Asn Thr
50 55 60

Leu Val Ala Asp Leu Ile Met Thr Leu Met Leu Pro Phe Lys Ile Leu
65 70 75 80

Ser Asp Ser His Leu Ala Pro Trp Gln Leu Arg Ala Phe Val Cys Arg
85 90 95

Phe Ser Ser Val Ile Phe Tyr Glu Thr Met Tyr Val Gly Ile Val Leu
100 105 110

Leu Gly Leu Ile Ala Phe Asp Arg Phe Leu Lys Ile Ile Arg Pro Leu
115 120 125

Arg Asn Ile Phe Leu Lys Lys Pro Val Phe Ala Lys Thr Val Ser Ile
130 135 140

Phe Ile Trp Val Phe Leu Val Phe Ile Ser Leu Pro Asn Met Ile Leu
145 150 155 160

Ser Asn Lys Glu Ala Thr Pro Ser Ser Val Lys Lys Cys Ala Ser Leu
165 170 175

Lys Gly Pro Leu Gly Leu Lys Trp His Gln Met Val Asn Asn Ile Cys
180 185 190

Gln Phe Ile Phe Trp Thr Gly Phe Ile Leu Met Leu Val Phe Tyr Val
195 200 205

Val Ile Ala Lys Lys Val Tyr Asp Ser Tyr Arg Lys Ser Lys Ser Lys
210 215 220

Asp Arg Lys Asn Asn Lys Lys Leu Glu Gly Lys Val Phe Val Val Val
225 230 235 240

Ala Val Phe Phe Val Cys Phe Ala Pro Phe His Phe Ala Arg Val Pro
245 250 255

Tyr Thr His Ser Gln Thr Asn Asn Lys Thr Asp Cys Arg Leu Gln Asn
260 265 270

Gln Leu Phe Ile Ala Lys Glu Thr Thr Leu Phe Leu Ala Ala Thr Asn
275 280 285

- 14 -

Ile Cys Met Asp Pro Leu Ile Tyr Ile Phe Leu Cys Lys Lys Phe Thr
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Glu Lys Leu Pro Cys Met Gln Gly Arg Lys Thr Thr Ala Ser Ser Gln
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cta ata ggc ctc cct ggt tta gaa gag gct cag ttc tgg ttg gcc ttc 96
 Leu Ile Gly Leu Pro Gly Leu Glu Glu Ala Gln Phe Trp Leu Ala Phe
 20 25 30

cca ttg tgc tcc ctc tac ctt att gct gtg cta ggt aac ttg aca atc 144
 Pro Leu Cys Ser Leu Tyr Leu Ile Ala Val Leu Gly Asn Leu Thr Ile
 35 40 45

atc tac att gtg cgg act gag cac agc ctg cat gag ccc atg tat ata 192
 Ile Tyr Ile Val Arg Thr Glu His Ser Leu His Glu Pro Met Tyr Ile
 50 55 60

ttt ctt tgc atg ctt tca ggc att gac atc ctc atc tcc acc tca tcc 240
 Phe Leu Cys Met Leu Ser Gly Ile Asp Ile Leu Ile Ser Thr Ser Ser
 65 70 75 80

atg ccc aaa atg ctg gcc atc ttc tgg ttc aat tcc act acc atc cag 288
 Met Pro Lys Met Leu Ala Ile Phe Trp Phe Asn Ser Thr Thr Ile Gln
 85 90 95

ttt gat gct tgt ctg cta cag atg ttt gcc atc cac tcc tta tct ggc 336
 Phe Asp Ala Cys Leu Leu Gln Met Phe Ala Ile His Ser Leu Ser Gly
 100 105 110

atg gaa tcc aca gtg ctg ctg gcc atg gct ttt gac cgc tat gtg gcc 384
 Met Glu Ser Thr Val Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala
 115 120 125

atc tgt cac cca ctg cgc cat gcc aca gta ctt acg ttg cct cgt gtc 432
 Ile Cys His Pro Leu Arg His Ala Thr Val Leu Thr Leu Pro Arg Val
 130 135 140

acc aaa att ggt gtg gct gct gtg gtg cgg ggg gct gca ctg atg gca 480
 Thr Lys Ile Gly Val Ala Ala Val Val Arg Gly Ala Ala Leu Met Ala
 145 150 155 160

ccc ctt cct gtc ttc atc aag cag ctg ccc ttc tgc cgc tcc aat atc 528
 Pro Leu Pro Val Phe Ile Lys Gln Leu Pro Phe Cys Arg Ser Asn Ile
 165 170 175

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180 185 190

gat gat atc cgg gtc aat gtc gtc tat ggc ctt atc gtc atc atc tcc 624
Asp Asp Ile Arg Val Asn Val Val Tyr Gly Leu Ile Val Ile Ile Ser
195 200 205

gcc att ggc ctg gac tca ctt ctc atc tcc ttc tca tat ctg ctt att 672
Ala Ile Gly Leu Asp Ser His Leu Ile Ser Phe Ser Tyr Leu Leu Ile
210 215 220

ctt aag act gtg ttg ggc ttg aca cgt gaa gcc cag gcc aag gca ttt 720
Leu Lys Thr Val Leu Leu Thr Arg Glu Ala Gln Ala Lys Ala Phe
225 230 235 240

ggc act tgc gtc tct cat gtg tgt gct gtg ttc ata ttc tat gta cct 768
Gly Thr Cys Val Ser His Val Cys Ala Val Phe Ile Phe Tyr Val Pro
245 250 255

ttc att gga ttg tcc atg gtg cat cgc ttt agc aag cgg cgt gac tct 816
Phe Ile Gly Leu Ser Met Val His Arg Phe Ser Lys Arg Arg Asp Ser
260 265 270

ccg ctg ccc gtc atc ttg gcc aat atc tat ctg ctg gtt cct cct gtg 864
Pro Leu Pro Val Ile Leu Ala Asn Ile Tyr Leu Leu Val Pro Pro Val
275 280 285

ctc aac cca att gtc tat gga gtg aag aca aag gag att cga cag cgc 912
Leu Asn Pro Ile Val Tyr Gly Val Lys Thr Lys Glu Ile Arg Gln Arg
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Pro Leu Cys Ser Leu Tyr Leu Ile Ala Val Leu Gly Asn Leu Thr Ile
35 40 45

Ile Tyr Ile Val Arg Thr Glu His Ser Leu His Glu Pro Met Tyr Ile
50 55 60

Phe Leu Cys Met Leu Ser Gly Ile Asp Ile Leu Ile Ser Thr Ser Ser
65 70 75 80

Met Pro Lys Met Leu Ala Ile Phe Trp Phe Asn Ser Thr Thr Ile Gln
85 90 95

Phe Asp Ala Cys Leu Leu Gln Met Phe Ala Ile His Ser Leu Ser Gly
100 105 110

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- 16 -

Met Glu Ser Thr Val Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala
 115 120 125

Ile Cys His Pro Leu Arg His Ala Thr Val Leu Thr Leu Pro Arg Val
 130 135 140

Thr Lys Ile Gly Val Ala Ala Val Val Arg Gly Ala Ala Leu Met Ala
 145 150 155 160

Pro Leu Pro Val Phe Ile Lys Gln Leu Pro Phe Cys Arg Ser Asn Ile
 165 170 175

Leu Ser His Ser Tyr Cys Leu His Gln Asp Val Met Lys Leu Ala Cys
 180 185 190

Asp Asp Ile Arg Val Asn Val Val Tyr Gly Leu Ile Val Ile Ile Ser
 195 200 205

Ala Ile Gly Leu Asp Ser Leu Leu Ile Ser Phe Ser Tyr Leu Leu Ile
 210 215 220

Leu Lys Thr Val Leu Gly Leu Thr Arg Glu Ala Gln Ala Lys Ala Phe
 225 230 235 240

Gly Thr Cys Val Ser His Val Cys Ala Val Phe Ile Phe Tyr Val Pro
 245 250 255

Phe Ile Gly Leu Ser Met Val His Arg Phe Ser Lys Arg Arg Asp Ser
 260 265 270

Pro Leu Pro Val Ile Leu Ala Asn Ile Tyr Leu Leu Val Pro Pro Val
 275 280 285

Leu Asn Pro Ile Val Tyr Gly Val Lys Thr Lys Glu Ile Arg Gln Arg
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ctg acc cag tct caa gat att cag ctc ctg gtc ttt gtg cta gtt tta 96
 Leu Thr Gln Ser Gln Asp Ile Gln Leu Leu Val Phe Val Leu Val Leu
 20 25 30

ata ttc tac ttc atc atc ctc cct gga aat ttt ctc att att ttc acc 144
 Ile Phe Tyr Phe Ile Ile Leu Pro Gly Asn Phe Leu Ile Ile Phe Thr
 35 40 45

ata aag tca gac cct ggg ctc aca gcc ccc ctc tat ttc ttt ctg ggc 192
 Ile Lys Ser Asp Pro Gly Leu Thr Ala Pro Leu Tyr Phe Phe Leu Gly
 50 55 60

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Asn Leu Ala Phe Leu Asp Ala Ser Tyr Ser Phe Ile Val Ala Pro Arg	
65 70 75 80	
atg ttg gtg gac ttc ctc tct gcg aag aag ata atc tcc tac aga ggc	288
Met Leu Val Asp Phe Leu Ser Ala Lys Lys Ile Ile Ser Tyr Arg Gly	
85 90 95	
tgc atc act cag ctc ttt ttc ttg cac ttc ctt gga gga ggg gag gga	336
Cys Ile Thr Gln Leu Phe Phe Leu His Phe Leu Gly Gly Gly Glu Gly	
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tta ctc ctt gtt gtg atg gcc ttt gac cgc tac atc gcc atc tgc cgg	384
Leu Leu Leu Val Val Met Ala Phe Asp Arg Tyr Ile Ala Ile Cys Arg	
115 120 125	
cct ctg cac tat cct act gtc atg aac cct aga acc tgc tat gca atg	432
Pro Leu His Tyr Pro Thr Val Met Asn Pro Arg Thr Cys Tyr Ala Met	
130 135 140	
atg ttg gct ctg tgg ctt ggg ggt ttt gtc cac tcc att atc cag gtg	480
Met Leu Ala Leu Trp Leu Gly Gly Phe Val His Ser Ile Ile Gln Val	
145 150 155 160	
gtc ctc atc ctc cgc ttg cct ttt tgt ggc cca aac cag ctg gac aac	528
Val Leu Ile Leu Arg Leu Pro Phe Cys Gly Pro Asn Gln Leu Asp Asn	
165 170 175	
ttc ttc tgt gat gtc cca cag gtc atc aag ctg gcc tgc acc gac aca	576
Phe Phe Cys Asp Val Pro Gln Val Ile Lys Leu Ala Cys Thr Asp Thr	
180 185 190	
ttt gtg gtg gag ctt ctg atg gtc ttc aac agt ggc ctg atg aca ctc	624
Phe Val Val Glu Leu Leu Met Val Phe Asn Ser Gly Leu Met Thr Leu	
195 200 205	
ctg tgc ttt ctg ggg ctt ctg gcc tcc tat gca gtc att ctt tgt cgc	672
Leu Cys Phe Leu Gly Leu Leu Ala Ser Tyr Ala Val Ile Leu Cys Arg	
210 215 220	
ata cga ggg tct tct tct gag gca aaa aac aag gcc atg tcc acg tgc	720
Ile Arg Gly Ser Ser Ser Glu Ala Lys Asn Lys Ala Met Ser Thr Cys	
225 230 235 240	
atc acc cat atc att gtt ata ttc ttc atg ttt gga cct ggc atc ttc	768
Ile Thr His Ile Ile Val Ile Phe Phe Met Phe Gly Pro Gly Ile Phe	
245 250 255	
atc tac acg cgc ccc ttc agg gct ttc cca gct gac aag gtg gtt tct	816
Ile Tyr Thr Arg Pro Phe Arg Ala Phe Pro Ala Asp Lys Val Val Ser	
260 265 270	
ctc ttc cac aca gtg att ttt cct ttg ttg aat cct gtc att tat acc	864
Leu Phe His Thr Val Ile Phe Pro Leu Leu Asn Pro Val Ile Tyr Thr	
275 280 285	
ctt cgc aac cag gaa gtg aaa gct tcc atg aaa aag gtg ttt aat aag	912
Leu Arg Asn Gln Glu Val Lys Ala Ser Met Lys Lys Val Phe Asn Lys	
290 295 300	
cac ata gcc tgaaaaaggg cgcaaaaaaa aaaagaataa aaatagactg	961
His Ile Ala	
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Ile Phe Tyr Phe Ile Ile Leu Pro Gly Asn Phe Leu Ile Ile Phe Thr
 35 40 45

Ile Lys Ser Asp Pro Gly Leu Thr Ala Pro Leu Tyr Phe Phe Leu Gly
 50 55 60

Asn Leu Ala Phe Leu Asp Ala Ser Tyr Ser Phe Ile Val Ala Pro Arg
 65 70 75 80

Met Leu Val Asp Phe Leu Ser Ala Lys Lys Ile Ile Ser Tyr Arg Gly
 85 90 95

Cys Ile Thr Gln Leu Phe Phe Leu His Phe Leu Gly Gly Gly Glu Gly
 100 105 110

Leu Leu Leu Val Val Met Ala Phe Asp Arg Tyr Ile Ala Ile Cys Arg
 115 120 125

Pro Leu His Tyr Pro Thr Val Met Asn Pro Arg Thr Cys Tyr Ala Met
 130 135 140

Met Leu Ala Leu Trp Leu Gly Gly Phe Val His Ser Ile Ile Gln Val
 145 150 155 160

Val Leu Ile Leu Arg Leu Pro Phe Cys Gly Pro Asn Gln Leu Asp Asn
 165 170 175

Phe Phe Cys Asp Val Pro Gln Val Ile Lys Leu Ala Cys Thr Asp Thr
 180 185 190

Phe Val Val Glu Leu Leu Met Val Phe Asn Ser Gly Leu Met Thr Leu
 195 200 205

Leu Cys Phe Leu Gly Leu Leu Ala Ser Tyr Ala Val Ile Leu Cys Arg
 210 215 220

Ile Arg Gly Ser Ser Ser Glu Ala Lys Asn Lys Ala Met Ser Thr Cys
 225 230 235 240

Ile Thr His Ile Ile Val Ile Phe Phe Met Phe Gly Pro Gly Ile Phe
 245 250 255

Ile Tyr Thr Arg Pro Phe Arg Ala Phe Pro Ala Asp Lys Val Val Ser
 260 265 270

Leu Phe His Thr Val Ile Phe Pro Leu Leu Asn Pro Val Ile Tyr Thr
 275 280 285

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Leu Arg Asn Gln Glu Val Lys Ala Ser Met Lys Lys Val Phe Asn Lys
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His Ile Ala
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 agaaaagagg aagcatgact gcagatcaga tcagttctct ttgtggatta tattttcagt 180
 aaaatgtatg gatctatctt ttccttggtc ttatatctag atcatgagac ttgactgagg 240
 ctgtatcctt atcctccatc catct atg gcg aac tat agc cat gca gct gac 292
 Met Ala Asn Tyr Ser His Ala Ala Asp
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aac att ttg caa aat ctc tgc cct cta aca gcc ttt ctg aaa ctg act 340
 Asn Ile Leu Gln Asn Leu Ser Pro Leu Thr Ala Phe Leu Lys Leu Thr
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tcc ttg ggt ttc ata ata gga gtc agc gtg gtg ggc aac ctc ctg atc 388
 Ser Leu Gly Phe Ile Ile Gly Val Ser Val Val Gly Asn Leu Leu Ile
 30 35 40

tcc att ttg cta gtg aaa gat aag acc ttg cat aga gca cct tac tac 436
 Ser Ile Leu Leu Val Lys Asp Lys Thr Leu His Arg Ala Pro Tyr Tyr
 45 50 55

ttc ctg ttg gat ctt tgc tgt tca gat atc ctc aga tct gca att tgt 484
 Phe Leu Leu Asp Leu Cys Cys Ser Asp Ile Leu Arg Ser Ala Ile Cys
 60 65 70

ttc cca ttt gtg ttc aac tct gtc aaa aat ggt tct acc tgg act tat 532
 Phe Pro Phe Val Phe Asn Ser Val Lys Asn Gly Ser Thr Trp Thr Tyr
 75 80 85

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 Gly Thr Leu Thr Cys Lys Val Ile Ala Phe Leu Gly Val Leu Ser Cys
 90 95 100 105

ttc cac act gct ttc atg ctc ttc tgc atc agt gtc acc aga tat tta 628
 Phe His Thr Ala Phe Met Leu Phe Cys Ile Ser Val Thr Arg Tyr Leu
 110 115 120

gct atc gcc cat cac cgc ttc tat aca aag agg ctg acc ttt tgg acg 676
 Ala Ile Ala His His Arg Phe Tyr Thr Lys Arg Leu Thr Phe Trp Thr
 125 130 135

tgt ctg gct gtg atc tgt atg gtg tgg act ctg tct gtg gcc atg gca 724
 Cys Leu Ala Val Ile Cys Met Val Trp Thr Leu Ser Val Ala Met Ala
 140 145 150

ttt ccc ccg gtt tta gac gtg ggc act tac tca ttc att agg gag gaa 772
 Phe Pro Pro Val Leu Asp Val Gly Thr Tyr Ser Phe Ile Arg Glu Glu
 155 160 165

gat caa tgc acc ttc caa cac cgc tcc ttc agg gct aat gat tcc tta 820
 Asp Gln Cys Thr Phe Gln His Arg Ser Phe Arg Ala Asn Asp Ser Leu
 170 175 180 185

gga ttt atg ctg ctt ctt gct ctc atc ctc cta gcc aca cag ctt gtc 868
 Gly Phe Met Leu Leu Leu Ala Leu Ile Leu Leu Ala Thr Gln Leu Val
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tac ctc aag ctg ata ttt ttc gtc cac gat cga aga aaa atg aag cca 916
 Tyr Leu Lys Leu Ile Phe Phe Val His Asp Arg Arg Lys Met Lys Pro
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gtc cag ttt gta gca gca gtc agc cag aac tgg act ttt cat ggt cct 964
 Val Gln Phe Val Ala Ala Val Ser Gln Asn Trp Thr Phe His Gly Pro
 220 225 230

gga gcc agt ggc cag gca gct gcc aat tgg cta gca gga ttt gga agg 1012
 Gly Ala Ser Gly Gln Ala Ala Ala Asn Trp Leu Ala Gly Phe Gly Arg
 235 240 245

ggt ccc aca cca ccc acc ttg ctg ggc atc agg caa aat gca aac acc 1060
 Gly Pro Thr Pro Pro Thr Leu Leu Gly Ile Arg Gln Asn Ala Asn Thr
 250 255 260 265

aca ggc aga aga agg cta ttg gtc tta gac gag ttc aaa atg gag aaa 1108
 Thr Gly Arg Arg Arg Leu Leu Val Leu Asp Glu Phe Lys Met Glu Lys
 270 275 280

aga atc agc aga atg ttc tat ata atg act ttt ctg ttt cta acc ttg 1156
 Arg Ile Ser Arg Met Phe Tyr Ile Met Thr Phe Leu Phe Leu Thr Leu
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 Trp Gly Pro Tyr Leu Val Ala Cys Tyr Trp Arg Val Phe Ala Arg Gly
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cct gta gta cca ggg gga ttt cta aca gct gct gtc tgg atg agt ttt 1252
 Pro Val Val Pro Gly Gly Phe Leu Thr Ala Ala Val Trp Met Ser Phe
 315 320 325

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gcc caa gca gga atc aat cct ttt gtc tgc att ttc tca aac agg gag 1300
 Ala Gln Ala Gly Ile Asn Pro Phe Val Cys Ile Phe Ser Asn Arg Glu
 330 335 340 345

ctg agg cgc tgt ttc agc aca acc ctt ctt tac tgc aga aaa tcc agg 1348
 Leu Arg Arg Cys Phe Ser Thr Thr Leu Leu Tyr Cys Arg Lys Ser Arg
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Val Ser Val Val Gly Asn Leu Leu Ile Ser Ile Leu Leu Val Lys Asp
 35 40 45

Lys Thr Leu His Arg Ala Pro Tyr Tyr Phe Leu Leu Asp Leu Cys Cys
 50 55 60

Ser Asp Ile Leu Arg Ser Ala Ile Cys Phe Pro Phe Val Phe Asn Ser
 65 70 75 80

Val Lys Asn Gly Ser Thr Trp Thr Tyr Gly Thr Leu Thr Cys Lys Val
 85 90 95

Ile Ala Phe Leu Gly Val Leu Ser Cys Phe His Thr Ala Phe Met Leu
 100 105 110

Phe Cys Ile Ser Val Thr Arg Tyr Leu Ala Ile Ala His His Arg Phe
 115 120 125

Tyr Thr Lys Arg Leu Thr Phe Trp Thr Cys Leu Ala Val Ile Cys Met
 130 135 140

Val Trp Thr Leu Ser Val Ala Met Ala Phe Pro Pro Val Leu Asp Val
 145 150 155 160

Gly Thr Tyr Ser Phe Ile Arg Glu Glu Asp Gln Cys Thr Phe Gln His
 165 170 175

Arg Ser Phe Arg Ala Asn Asp Ser Leu Gly Phe Met Leu Leu Leu Ala
 180 185 190

Leu Ile Leu Leu Ala Thr Gln Leu Val Tyr Leu Lys Leu Ile Phe Phe
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Val His Asp Arg Arg Lys Met Lys Pro Val Gln Phe Val Ala Ala Val
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Ser Gln Asn Trp Thr Phe His Gly Pro Gly Ala Ser Gly Gln Ala Ala
 225 230 235 240

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Gln	Tyr	Cys	Gly	Tyr	Ala	Pro	His	Val	Arg	Ser	Cys	Lys	Pro	Asn	Thr			
			20					25					30					
gat	gga	att	tca	tct	cta	gag	aat	ctc	ttg	gca	agc	att	att	cag	aga	144		
Asp	Gly	Ile	Ser	Ser	Leu	Glu	Asn	Leu	Leu	Ala	Ser	Ile	Ile	Gln	Arg			
		35					40					45						
gta	ttt	gtc	tgg	ggt	gta	tct	gca	ggt	acc	tgc	ttt	gga	aac	att	ttt	192		
Val	Phe	Val	Trp	Val	Val	Ser	Ala	Val	Thr	Cys	Phe	Gly	Asn	Ile	Phe			
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gtc	att	tgc	atg	cga	cct	tat	atc	agg	tct	gag	aac	aag	ctg	tat	gcc	240		
Val	Ile	Cys	Met	Arg	Pro	Tyr	Ile	Arg	Ser	Glu	Asn	Lys	Leu	Tyr	Ala			
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atg	tca	atc	att	tct	ctc	tgc	tgt	gcc	gac	tgc	tta	atg	gga	ata	tat	288		
Met	Ser	Ile	Ile	Ser	Leu	Cys	Cys	Ala	Asp	Cys	Leu	Met	Gly	Ile	Tyr			
				85					90					95				

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tta ttc gtg atc gga ggc ttt gac cta aag ttt cgt gga gaa tac aat	336
Leu Phe Val Ile Gly Gly Phe Asp Leu Lys Phe Arg Gly Glu Tyr Asn	
100 105 110	
aag cat gcg cag ctg tgg atg gag agt act cat tgt cag ctt gta gga	384
Lys His Ala Gln Leu Trp Met Glu Ser Thr His Cys Gln Leu Val Gly	
115 120 125	
tct ttg gcc att ctg tcc aca gaa gta tca gtt tta ctg tta aca ttt	432
Ser Leu Ala Ile Leu Ser Thr Glu Val Ser Val Leu Leu Leu Thr Phe	
130 135 140	
ctg aca ttg gaa aaa tac atc tgc att gtc tat cct ttt aga tgt gtg	480
Leu Thr Leu Glu Lys Tyr Ile Cys Ile Val Tyr Pro Phe Arg Cys Val	
145 150 155 160	
aga cct gga aaa tgc aga aca att aca gtt ctg att ctc att tgg att	528
Arg Pro Gly Lys Cys Arg Thr Ile Thr Val Leu Ile Leu Ile Trp Ile	
165 170 175	
act ggt ttt ata gtg gct ttc att cca ttg agc aat aag gaa ttt ttc	576
Thr Gly Phe Ile Val Ala Phe Ile Pro Leu Ser Asn Lys Glu Phe Phe	
180 185 190	
aaa aac tac tat ggc acc aat gga gta tgc ttc cct ctt cat tca gaa	624
Lys Asn Tyr Tyr Gly Thr Asn Gly Val Cys Phe Pro Leu His Ser Glu	
195 200 205	
gat aca gaa agt att gga gcc cag att tat tca gtg gca att ttt ctt	672
Asp Thr Glu Ser Ile Gly Ala Gln Ile Tyr Ser Val Ala Ile Phe Leu	
210 215 220	
ggt att aat ttg gcc gca ttt atc atc ata gtt ttt tcc tat gga agc	720
Gly Ile Asn Leu Ala Ala Phe Ile Ile Ile Val Phe Ser Tyr Gly Ser	
225 230 235 240	
atg ttt tat agt gtt cat caa agt gcc ata aca gca act gaa ata cgg	768
Met Phe Tyr Ser Val His Gln Ser Ala Ile Thr Ala Thr Glu Ile Arg	
245 250 255	
aat caa gtt aaa aaa gag atg atc ctt gcc aaa cgt ttt ttc ttt ata	816
Asn Gln Val Lys Lys Glu Met Ile Leu Ala Lys Arg Phe Phe Phe Ile	
260 265 270	
gta ttt act gat gca tta tgc tgg ata ccc att ttt gta gtg aaa ttt	864
Val Phe Thr Asp Ala Leu Cys Trp Ile Pro Ile Phe Val Val Lys Phe	
275 280 285	
ctt tca ctg ctt cag gta gaa ata cca ggt acc ata acc tct tgg gta	912
Leu Ser Leu Leu Gln Val Glu Ile Pro Gly Thr Ile Thr Ser Trp Val	
290 295 300	
gtg att ttt att ctg ccc att aac agt gct ttg aac cca att ctc tat	960
Val Ile Phe Ile Leu Pro Ile Asn Ser Ala Leu Asn Pro Ile Leu Tyr	
305 310 315 320	
act ctg acc aca aga cca ttt aaa gaa atg att cat cgg ttt tgg tat	1008
Thr Leu Thr Thr Arg Pro Phe Lys Glu Met Ile His Arg Phe Trp Tyr	
325 330 335	
aac tac aga caa aga aaa tct atg gac agc aaa ggt cag aaa aca tat	1056
Asn Tyr Arg Gln Arg Lys Ser Met Asp Ser Lys Gly Gln Lys Thr Tyr	
340 345 350	

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gct cca tca ttc atc tgg gtg gaa atg tgg cca ctg cag gag atg cca 1104
 Ala Pro Ser Phe Ile Trp Val Glu Met Trp Pro Leu Gln Glu Met Pro
 355 360 365

cct gag tta atg aag ccg gac ctt ttc aca tac ccc tgt gaa atg tca 1152
 Pro Glu Leu Met Lys Pro Asp Leu Phe Thr Tyr Pro Cys Glu Met Ser
 370 375 380

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<213> Homo sapiens

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Asp Gly Ile Ser Ser Leu Glu Asn Leu Leu Ala Ser Ile Ile Gln Arg
 35 40 45

Val Phe Val Trp Val Val Ser Ala Val Thr Cys Phe Gly Asn Ile Phe
 50 55 60

Val Ile Cys Met Arg Pro Tyr Ile Arg Ser Glu Asn Lys Leu Tyr Ala
 65 70 75 80

Met Ser Ile Ile Ser Leu Cys Cys Ala Asp Cys Leu Met Gly Ile Tyr
 85 90 95

Leu Phe Val Ile Gly Gly Phe Asp Leu Lys Phe Arg Gly Glu Tyr Asn
 100 105 110

Lys His Ala Gln Leu Trp Met Glu Ser Thr His Cys Gln Leu Val Gly
 115 120 125

Ser Leu Ala Ile Leu Ser Thr Glu Val Ser Val Leu Leu Leu Thr Phe
 130 135 140

Leu Thr Leu Glu Lys Tyr Ile Cys Ile Val Tyr Pro Phe Arg Cys Val
 145 150 155 160

Arg Pro Gly Lys Cys Arg Thr Ile Thr Val Leu Ile Leu Ile Trp Ile
 165 170 175

Thr Gly Phe Ile Val Ala Phe Ile Pro Leu Ser Asn Lys Glu Phe Phe
 180 185 190

Lys Asn Tyr Tyr Gly Thr Asn Gly Val Cys Phe Pro Leu His Ser Glu
 195 200 205

Asp Thr Glu Ser Ile Gly Ala Gln Ile Tyr Ser Val Ala Ile Phe Leu
 210 215 220

Gly Ile Asn Leu Ala Ala Phe Ile Ile Ile Val Phe Ser Tyr Gly Ser
 225 230 235 240

- 25 -

Met Phe Tyr Ser Val His Gln Ser Ala Ile Thr Ala Thr Glu Ile Arg
245 250 255

Asn Gln Val Lys Lys Glu Met Ile Leu Ala Lys Arg Phe Phe Phe Ile
260 265 270

Val Phe Thr Asp Ala Leu Cys Trp Ile Pro Ile Phe Val Val Lys Phe
275 280 285

Leu Ser Leu Leu Gln Val Glu Ile Pro Gly Thr Ile Thr Ser Trp Val
290 295 300

Val Ile Phe Ile Leu Pro Ile Asn Ser Ala Leu Asn Pro Ile Leu Tyr
305 310 315 320

Thr Leu Thr Thr Arg Pro Phe Lys Glu Met Ile His Arg Phe Trp Tyr
325 330 335

Asn Tyr Arg Gln Arg Lys Ser Met Asp Ser Lys Gly Gln Lys Thr Tyr
340 345 350

Ala Pro Ser Phe Ile Trp Val Glu Met Trp Pro Leu Gln Glu Met Pro
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Pro Glu Leu Met Lys Pro Asp Leu Phe Thr Tyr Pro Cys Glu Met Ser
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gag ctg cac ggc caa gag agt cac aat tca ggc aac agg agc gac ggg 99
Glu Leu His Gly Gln Glu Ser His Asn Ser Gly Asn Arg Ser Asp Gly
15 20 25

cca gga aag aac acc acc ctt cac aat gaa ttt gac aca att gtc ttg 147
Pro Gly Lys Asn Thr Thr Leu His Asn Glu Phe Asp Thr Ile Val Leu
30 35 40 45

cca gtg ctt tat ctc att ata ttt gtg gca agc atc ttg ctg aat ggt 195
Pro Val Leu Tyr Leu Ile Ile Phe Val Ala Ser Ile Leu Leu Asn Gly
50 55 60

tta gca gtg tgg atc ttc ttc cac att agg aat aaa acc agc ttc ata 243
Leu Ala Val Trp Ile Phe Phe His Ile Arg Asn Lys Thr Ser Phe Ile
65 70 75

ttc tat ctc aaa aac ata gtg gtt gca gac ctc ata atg acg ctg aca 291
Phe Tyr Leu Lys Asn Ile Val Val Ala Asp Leu Ile Met Thr Leu Thr
80 85 90

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ttt cca ttt cga ata gtc cat gat gca gga ttt gga cct tgg tac ttc	339
Phe Pro Phe Arg Ile Val His Asp Ala Gly Phe Gly Pro Trp Tyr Phe	
95 100 105	
aag ttt att ctc tgc aga tac act tca gtt ttg ttt tat gca aac atg	387
Lys Phe Ile Leu Cys Arg Tyr Thr Ser Val Leu Phe Tyr Ala Asn Met	
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tat act tcc atc gtg ttc ctt ggg ctg ata agc att gat cgc tat ctg	435
Tyr Thr Ser Ile Val Phe Leu Gly Leu Ile Ser Ile Asp Arg Tyr Leu	
130 135 140	
aag gtg gtc aag cca ttt ggg gac tct cgg atg tac agc ata acc ttc	483
Lys Val Val Lys Pro Phe Gly Asp Ser Arg Met Tyr Ser Ile Thr Phe	
145 150 155	
acg aag gtt tta tct gtt tgt gtt tgg gtg atc atg gct gtt ttg tct	531
Thr Lys Val Leu Ser Val Cys Val Trp Val Ile Met Ala Val Leu Ser	
160 165 170	
ttg cca aac atc atc ctg aca aat ggt cag cca aca gag gac aat atc	579
Leu Pro Asn Ile Ile Leu Thr Asn Gly Gln Pro Thr Glu Asp Asn Ile	
175 180 185	
cat gac tgc tca aaa ctt aaa agt cct ttg ggg gtc aaa tgg cat acg	627
His Asp Cys Ser Lys Lys Ser Pro Leu Gly Val Lys Trp His Thr	
190 195 200 205	
gca gtc acc tat gtg aac agc tgc ttg ttt gtg gcc gtg ctg gtg att	675
Ala Val Thr Tyr Val Asn Ser Cys Leu Phe Val Ala Val Leu Val Ile	
210 215 220	
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Leu Ile Gly Cys Tyr Ile Ala Ile Ser Arg Tyr Ile His Lys Ser Ser	
225 230 235	
agg caa ttc ata agt cag tca agc cga aag cga aaa cat aac cag agc	771
Arg Gln Phe Ile Ser Gln Ser Ser Arg Lys Arg Lys His Asn Gln Ser	
240 245 250	
atc agg gtt gtt gtg gct gtg ttt ttt acc tgc ttt cta cca tat cac	819
Ile Arg Val Val Val Ala Val Phe Phe Thr Cys Phe Leu Pro Tyr His	
255 260 265	
ttg tgc aga att cct ttt act ttt agt cac tta gac agg ctt tta gat	867
Leu Cys Arg Ile Pro Phe Thr Phe Ser His Leu Asp Arg Leu Leu Asp	
270 275 280 285	
gaa tct gca caa aaa atc cta tat tac tgc aaa gaa att aca ctt ttc	915
Glu Ser Ala Gln Lys Ile Leu Tyr Tyr Cys Lys Glu Ile Thr Leu Phe	
290 295 300	
ttg tct gcg tgt aat gtt tgc ctg gat cca ata att tac ttt ttc atg	963
Leu Ser Ala Cys Asn Val Cys Leu Asp Pro Ile Ile Tyr Phe Phe Met	
305 310 315	
tgt agg tca ttt tca aga agg ctg ttc aaa aaa tca aat atc aga acc	1011
Cys Arg Ser Phe Ser Arg Arg Leu Phe Lys Lys Ser Asn Ile Arg Thr	
320 325 330	
agg agt gaa agc atc aga tca ctg caa agt gtg aga aga tcg gaa gtt	1059
Arg Ser Glu Ser Ile Arg Ser Leu Gln Ser Val Arg Arg Ser Glu Val	
335 340 345	

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ctc ata tat tat gat tat act gat gtg tag gcctttttatt gtttggttga 1109
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 35 40 45
 Tyr Leu Ile Ile Phe Val Ala Ser Ile Leu Leu Asn Gly Leu Ala Val
 50 55 60
 Trp Ile Phe Phe His Ile Arg Asn Lys Thr Ser Phe Ile Phe Tyr Leu
 65 70 75 80
 Lys Asn Ile Val Val Ala Asp Leu Ile Met Thr Leu Thr Phe Pro Phe
 85 90 95
 Arg Ile Val His Asp Ala Gly Phe Gly Pro Trp Tyr Phe Lys Phe Ile
 100 105 110
 Leu Cys Arg Tyr Thr Ser Val Leu Phe Tyr Ala Asn Met Tyr Thr Ser
 115 120 125
 Ile Val Phe Leu Gly Leu Ile Ser Ile Asp Arg Tyr Leu Lys Val Val
 130 135 140
 Lys Pro Phe Gly Asp Ser Arg Met Tyr Ser Ile Thr Phe Thr Lys Val
 145 150 155 160
 Leu Ser Val Cys Val Trp Val Ile Met Ala Val Leu Ser Leu Pro Asn
 165 170 175
 Ile Ile Leu Thr Asn Gly Gln Pro Thr Glu Asp Asn Ile His Asp Cys
 180 185 190
 Ser Lys Leu Lys Ser Pro Leu Gly Val Lys Trp His Thr Ala Val Thr
 195 200 205
 Tyr Val Asn Ser Cys Leu Phe Val Ala Val Leu Val Ile Leu Ile Gly
 210 215 220
 Cys Tyr Ile Ala Ile Ser Arg Tyr Ile His Lys Ser Ser Arg Gln Phe
 225 230 235 240
 Ile Ser Gln Ser Ser Arg Lys Arg Lys His Asn Gln Ser Ile Arg Val
 245 250 255
 Val Val Ala Val Phe Phe Thr Cys Phe Leu Pro Tyr His Leu Cys Arg
 260 265 270

- 28 -

Ile Pro Phe Thr Phe Ser His Leu Asp Arg Leu Leu Asp Glu Ser Ala
 275 280 285

Gln Lys Ile Leu Tyr Tyr Cys Lys Glu Ile Thr Leu Phe Leu Ser Ala
 290 295 300

Cys Asn Val Cys Leu Asp Pro Ile Ile Tyr Phe Phe Met Cys Arg Ser
 305 310 315 320

Phe Ser Arg Arg Leu Phe Lys Lys Ser Asn Ile Arg Thr Arg Ser Glu
 325 330 335

Ser Ile Arg Ser Leu Gln Ser Val Arg Arg Ser Glu Val Leu Ile Tyr
 340 345 350

Tyr Asp Tyr Thr Asp Val
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<220>

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 Met Leu Ala Asn Ser
 1 5

tcc tca acc aac agt tct gtt ctc ccg tgt cct gac tac cga cct acc 104
 Ser Ser Thr Asn Ser Ser Val Leu Pro Cys Pro Asp Tyr Arg Pro Thr
 10 15 20

cac cgc ctg cac ttg gtg gtc tac agc ttg gtg ctg gct gcc ggg ctc 152
 His Arg Leu His Leu Val Val Tyr Ser Leu Val Leu Ala Ala Gly Leu
 25 30 35

ccc ctc aac gcg cta gcc ctc tgg gtc ttc ctg cgc gcg ctg cgc gtg 200
 Pro Leu Asn Ala Leu Ala Leu Trp Val Phe Leu Arg Ala Leu Arg Val
 40 45 50

cac tcg gtg gtg agc gtg tac atg tgt aac ctg gcg gcc agc gac ctg 248
 His Ser Val Val Ser Val Tyr Met Cys Asn Leu Ala Ala Ser Asp Leu
 55 60 65

ctc ttc acc ctc tcg ctg ccc gtt cgt ctc tcc tac tac gca ctg cac 296
 Leu Phe Thr Leu Ser Leu Pro Val Arg Leu Ser Tyr Tyr Ala Leu His
 70 75 80 85

cac tgg ccc ttc ccc gac ctc ctg tgc cag acg acg ggc gcc atc ttc 344
 His Trp Pro Phe Pro Asp Leu Leu Cys Gln Thr Thr Gly Ala Ile Phe
 90 95 100

cag atg aac atg tac ggc agc tgc atc ttc ctg atg ctc atc aac gtg 392
 Gln Met Asn Met Tyr Gly Ser Cys Ile Phe Leu Met Leu Ile Asn Val
 105 110 115

gac cgc tac gcc gcc atc gtg cac ccg ctg cga ctg cgc cac ctg cgg 440
 Asp Arg Tyr Ala Ala Ile Val His Pro Leu Arg Leu Arg His Leu Arg
 120 125 130

- 29 -

cgg ccc cgc gtg gcg cgg ctg ctc tgc ctg ggc gtg tgg gcg ctc atc	488
Arg Pro Arg Val Ala Arg Leu Leu Cys Leu Gly Val Trp Ala Leu Ile	
135 140 145	
ctg gtg ttt gcc gtg ccc gcc gcc cgc gtg cac agg ccc tcg cgt tgc	536
Leu Val Phe Ala Val Pro Ala Ala Arg Val His Arg Pro Ser Arg Cys	
150 155 160 165	
cgc tac cgg gac ctc gag gtg cgc cta tgc ttc gag agc ttc agc gac	584
Arg Tyr Arg Asp Leu Glu Val Arg Leu Cys Phe Glu Ser Phe Ser Asp	
170 175 180	
gag ctg tgg aaa ggc agg ctg ctg ccc ctc gtg ctg ctg gcc gag gcg	632
Glu Leu Trp Lys Gly Arg Leu Leu Pro Leu Val Leu Leu Ala Glu Ala	
185 190 195	
ctg ggc ttc ctg ctg ccc ctg gcg gcg gtg gtc tac tcg tcg ggc cga	680
Leu Gly Phe Leu Leu Pro Leu Ala Ala Val Val Tyr Ser Ser Gly Arg	
200 205 210	
gtc ttc tgg acg ctg gcg cgc ccc gac gcc acg cag agc cag cgg cgg	728
Val Phe Trp Thr Leu Ala Arg Pro Asp Ala Thr Gln Ser Gln Arg Arg	
215 220 225	
cgg aag acc gtg cgc ctc ctg ctg gct aac ctc gtc atc ttc ctg ctg	776
Arg Lys Thr Val Arg Leu Leu Leu Ala Asn Leu Val Ile Phe Leu Leu	
230 235 240 245	
tgc ttc gtg ccc tac aac agc acg ctg gcg gtc tac ggg ctg ctg cgg	824
Cys Phe Val Pro Tyr Asn Ser Thr Leu Ala Val Tyr Gly Leu Leu Arg	
250 255 260	
agc aag ctg gtg gcg gcc agc gtg cct gcc cgc gat cgc gtg cgc ggg	872
Ser Lys Leu Val Ala Ala Ser Val Pro Ala Arg Asp Arg Val Arg Gly	
265 270 275	
gtg ctg atg gtg atg gtg ctg ctg gcc gcc gcc aac tgc gtg ctg gac	920
Val Leu Met Val Met Val Leu Leu Ala Gly Ala Asn Cys Val Leu Asp	
280 285 290	
ccg ctg gtg tac tac ttt agc gcc gag gcc ttc cgc aac acc ctg cgc	968
Pro Leu Val Tyr Tyr Phe Ser Ala Glu Gly Phe Arg Asn Thr Leu Arg	
295 300 305	
ggc ctg ggc act ccg cac cgg gcc agg acc tcg gcc acc aac ggg acg	1016
Gly Leu Gly Thr Pro His Arg Ala Arg Thr Ser Ala Thr Asn Gly Thr	
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Arg Ala Ala Leu Ala Gln Ser Glu Arg Ser Ala Val Thr Thr Asp Ala	
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acc agg ccg gat gcc gcc agt cag ggg ctg ctc cga ccc tcc gac tcc	1112
Thr Arg Pro Asp Ala Ala Ser Gln Gly Leu Leu Arg Pro Ser Asp Ser	
345 350 355	
cac tct ctg tct tcc ttc aca cag tgt ccc cag gat tcc gcc ctc	1157
His Ser Leu Ser Ser Phe Thr Gln Cys Pro Gln Asp Ser Ala Leu	
360 365 370	
tgaacacaca tgccattgcg ctgtccgtgc ccgactccca acgcctctcg ttctgggagg	1217
cttacagggt gtacacacaa gaaggtgggc tgggcacttg gacctttggg tggcaattcc	1277

- 30 -

agcttagcaa cgcagaagag tacaaagtgt ggaagccagg gccagggaa ggcagtgctg 1337
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 gagttcatgt ctaacttctt ccagggcat tatgtacagt gctttttatt actgtgggga 2417
 gagggcagt ctaaataaat taatcactac tgataaaaaa aaaaaaaaaa aaaaaaaaaa 2477
 aaa 2480

<210> 20

<211> 372

<212> PRT

<213> Homo sapiens

<400> 20

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Asp	Tyr	Arg	Pro	Thr	His	Arg	Leu	His	Leu	Val	Val	Tyr	Ser	Leu	Val
			20					25					30		
Leu	Ala	Ala	Gly	Leu	Pro	Leu	Asn	Ala	Leu	Ala	Leu	Trp	Val	Phe	Leu
			35				40					45			
Arg	Ala	Leu	Arg	Val	His	Ser	Val	Val	Ser	Val	Tyr	Met	Cys	Asn	Leu
		50				55					60				
Ala	Ala	Ser	Asp	Leu	Leu	Phe	Thr	Leu	Ser	Leu	Pro	Val	Arg	Leu	Ser
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- 32 -

<223> Description of Artificial Sequence: Primer LW1282

<400> 21

taatacctgc actgcccac

19

<210> 22

<211> 22

<212> DNA

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<223> Description of Artificial Sequence: Primer LW 1283

<400> 22

tctttccttc tcttctcact cc

22

<210> 23

<211> 32

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer LW 1373

<400> 23

gcataagctt atgctaacac tgaataaaac ag

32

<210> 24

<211> 30

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer LW1374

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<210> 25

<211> 9

<212> PRT

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<223> Description of Artificial Sequence: Peptide

<400> 25

Ala Pro Arg Thr Pro Gly Gly Arg Arg

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5

<210> 26

<211> 32

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer LW1248

- 33 -

<400> 26
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<223> Description of Artificial Sequence: Primer LW1249

<400> 27
gcatggatcc ggaaaagaag gagaagaaag 30

<210> 28
<211> 18
<212> DNA
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<223> Description of Artificial Sequence: Primer LW1278

<400> 28
accgctgcct ttttagtc 18

<210> 29
<211> 23
<212> DNA
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<223> Description of Artificial Sequence: Primer LW1279

<400> 29
ccttctttct gggtacataa gtc 23

<210> 30
<211> 30
<212> DNA
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<223> Description of Artificial Sequence: Primer LW1405

<400> 30
aagcataaca tggatgaaac aggaaatctg 30

<210> 31
<211> 29
<212> DNA
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<223> Description of Artificial Sequence: Primer LW1406

<400> 31
aagcataact atactttaca tatttcttc 29

- 34 -

<210> 32
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<212> DNA
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<220>
<223> Description of Artificial Sequence: Primer LW1280

<400> 32
tctgcacaca gctcttccat gg 22

<210> 33
<211> 22
<212> DNA
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<220>
<223> Description of Artificial Sequence: Primer LW1281

<400> 33
tcccttggtcc agttggttga gg 22

<210> 34
<211> 30
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<220>
<223> Description of Artificial Sequence: Primer LW1385

<400> 34
gcataagctt ccatggaact tcataacctg 30

<210> 35
<211> 30
<212> DNA
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<220>
<223> Description of Artificial Sequence: Primer LW1386

<400> 35
gcatctcgag ttacccccac agcgctgcag 30

<210> 36
<211> 29
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<223> Description of Artificial Sequence: Primer LW1329

<400> 36
gcatctcgag tcagcctaag gttatgttg 29

<210> 37
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<212> DNA

- 35 -

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer LW1377

<400> 37

gcataagctt atgaacacca cagtgatgc

29

<210> 38

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer LW1387

<400> 38

gagaaatatt tttctaaaaa aacctgtttt tgcaaaaacg g

41

<210> 39

<211> 41

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer LW1388

<400> 39

ccgtttttgc aaaaacaggt ttttttagaa aaatatttct c

41

<210> 40

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer LW1314

<400> 40

gcatgaattc ccaccttcac catctacctc

30

<210> 41

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer LW1315

<400> 41

gcatggatcc gaagaccaa aagaccag

29

<210> 42

<211> 30

<212> DNA

<213> Artificial Sequence

- 36 -

<220>
<223> Description of Artificial Sequence: Primer LW1326

<400> 42
gcatgaattc atgatggtag atcccaatgg 30

<210> 43
<211> 27
<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer LW1327

<400> 43
gcatctcgag cctagggtc tgaagcg 27

<210> 44
<211> 42
<212> DNA
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<220>
<223> Description of Artificial Sequence: Primer LW1415

<400> 44
ccatgtatat atttctttgc atgctttcag gcattgacat cc 42

<210> 45
<211> 42
<212> DNA
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<220>
<223> Description of Artificial Sequence: Primer LW1416

<400> 45
ggatgtcaat gcctgaaagc atgcaaagaa atatatacat gg 42

<210> 46
<211> 30
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<223> Description of Artificial Sequence: Primer LW1308

<400> 46
gcatgaattc actcacttct catctccttc 30

<210> 47
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<223> Description of Artificial Sequence: Primer LW1309

<400> 47

- 37 -

gcatggatcc aatctccttt gtcttcactc 30

<210> 48
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<400> 48
gatcggatcc atggaaagcg agaacag 27

<210> 49
<211> 35
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<223> Description of Artificial Sequence: Primer LW1325

<400> 49
gacccctcgag tcaggctatg tgcttattaa acacc 35

<210> 50
<211> 29
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<220>
<223> Description of Artificial Sequence: Primer LW1306

<400> 50
gcatgaattc ttctacttca tcatcctcc 29

<210> 51
<211> 28
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<223> Description of Artificial Sequence: Primer LW1307

<400> 51
gcatggatcc aaaggccatc acaacaag 28

<210> 52
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<220>
<223> Description of Artificial Sequence: Primer GV599

<400> 52
ggcagaagaa ggctattggt cttagacgag 30

- 38 -

<210> 53
<211> 22
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<220>
<223> Description of Artificial Sequence: Primer GV600

<400> 53
ctgaaacagc gcctcagctc cc 22

<210> 54
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<223> Description of Artificial Sequence: Primer LW1482

<400> 54
agctatggcg aactatagcc atgcagc 27

<210> 55
<211> 27
<212> DNA
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<220>
<223> Description of Artificial Sequence: Primer LW148

<400> 55
agtcctcata taacacagta aggttcc 27

<210> 56
<211> 28
<212> DNA
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<223> Description of Artificial Sequence: Primer LW1310

<400> 56
gcatgaattc gcagaagaag gctattgg 28

<210> 57
<211> 29
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<220>
<223> Description of Artificial Sequence: Primer LW1311

<400> 57
gcatggatcc gcagtaaaga agggttgtg 29

<210> 58
<211> 19

- 39 -

<212> DNA
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<220>
<223> Description of Artificial Sequence: Primer LW1442

<400> 58
gccattctgt ccacagaag 19

<210> 59
<211> 19
<212> DNA
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<223> Description of Artificial Sequence: Primer LW1443

<400> 59
tcagttgctg ttatggcac 19

<210> 60
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<212> DNA
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<220>
<223> Description of Artificial Sequence: Primer LW1440

<400> 60
aagcggatgt ttagacctct tgtg
24

<210> 61
<211> 23
<212> DNA
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<220>
<223> Description of Artificial Sequence: Primer LW1441

<400> 61
aacagtcacg aataggaatt gag 23

<210> 62
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer LW1472

<400> 62
gcatgaattc tgccatgtca atcatttctc tc 32

<210> 63
<211> 31

- 40 -

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer LW1473

<400> 63
gcatggatcc gttctgcatt ttccaggtct c 31

<210> 64
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer LW1411

<400> 64
gcatgaattc tgccaaacat catcctgac 29

<210> 65
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer LW1412

<400> 65
gcatggatcc tacacagcca caacaaccc 29

<210> 66
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer LW1448

<400> 66
aagcggtagc atgtagcca acagctcttc 30

<210> 67
<211> 29
<212> DNA
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<220>
<223> Description of Artificial Sequence: Primer LW1449

<400> 67
aagctctaga tcagagggcg gaatcctgg 29

<210> 68
<211> 43
<212> DNA

- 41 -

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer 217A

<400> 68

taggtcggta gtcaggacac gggagaacag aactgttggt tga

43

<210> 69

<211> 52

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer 217B

<400> 69

gccctctggtg cggtttagat ccagaatgcc cattttctgt tccatctaac ca

52

<210> 70

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer LW1480

<400> 70

ggttctacct ggacttatgg

20

<210> 71

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer LW1481

<400> 71

taatgaatga gtaagtgcc

20

<210> 72

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer CON103a

<400> 72

tttattaata ttggaaggga caaactggag agcacagaac at

42

<210> 73

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer CON103b

<400> 73

- 42 -

aaagccacca tggaagccat gccaaagatg atgctgggca agaa

44

<210> 74

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer 1332

<400> 74

tcctactgtc atgaaccc

18

<210> 75

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer 1333

<400> 75

cagaagaagt tgtccagc

18